



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122044

To: Mary Zeman
Location: rem/2d61/2c70
Art Unit: 1631
Monday, May 17, 2004

Case Serial Number: 10/621401

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

STIC-Biotech/ChemLib

122044

From: Zeman, Mary
Sent: Friday, May 14, 2004 9:52 AM
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Subject: seq search

please search in 10/621401

Please run a regular search of SEQ ID NO: 145 in regular AND interference files

Please run an OLIGO search of SEQ ID NO: 145 in regular files.

Paper printout please

thank you

Mary K. Zeman
Primary Examiner, 1631
571-272-0723
Remsen 2D61
MAILBOX: REM 2C70
mary.zeman@uspto.gov

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 5-17
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:35:53 ; Search time 60 Seconds
(without alignments)
913.570 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLASGFLVWLSLGGGLAQ.....PFMNSQRAACICAEKEEKL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|-----------|-------------|
| 1 | 1064 | 99.8 | 194 | 5 | ABP62920 | Human pol |
| 2 | 1064 | 99.8 | 194 | 6 | ADA57403 | Human sec |
| 3 | 1064 | 99.8 | 194 | 6 | ADA56921 | Human sec |
| 4 | 1064 | 99.8 | 194 | 6 | ADA41278 | Human sec |
| 5 | 1064 | 99.8 | 194 | 6 | ADA40769 | Human sec |
| 6 | 1064 | 99.8 | 194 | 6 | ABO13978 | Novel hum |
| 7 | 1064 | 99.8 | 194 | 6 | ABR48024 | Human sec |
| 8 | 1064 | 99.8 | 194 | 6 | ABR47739 | Human sec |
| 9 | 1064 | 99.8 | 195 | 2 | AAy27572 | Human sec |
| 10 | 655.5 | 61.5 | 335 | 7 | ADSO8422 | Novel pro |
| 11 | 467 | 43.8 | 192 | 3 | AAy88282 | Murine TA |
| 12 | 467 | 43.8 | 192 | 5 | ABO8151 | Murine GX |
| 13 | 458 | 43.0 | 189 | 3 | AAy88271 | Human TAN |
| 14 | 458 | 43.0 | 189 | 3 | AAy87282 | Human sig |
| 15 | 458 | 43.0 | 189 | 4 | AAO66607 | Human pro |
| 16 | 458 | 43.0 | 189 | 4 | AAU12291 | Human pro |
| 17 | 458 | 43.0 | 189 | 4 | AAy88353 | Human mem |
| 18 | 458 | 43.0 | 189 | 4 | AAy881285 | Human APP |
| 19 | 458 | 43.0 | 189 | 5 | AAU36906 | Human SPL |
| 20 | 458 | 43.0 | 189 | 5 | ABO81150 | Human GXI |
| 21 | 458 | 43.0 | 189 | 5 | ABP64382 | Human ORF |
| 22 | 458 | 43.0 | 189 | 6 | ABO17735 | Novel hum |
| 23 | 458 | 43.0 | 189 | 6 | ABU80989 | Human pro |
| 24 | 458 | 43.0 | 189 | 6 | ABU66689 | Human pro |
| 25 | 458 | 43.0 | 189 | 6 | ABU59770 | Novel sec |

ALIGNMENTS

RESULT 1

ABP62920

ID ABP62920 standard; protein; 194 AA.

AC ABP62920;

DT 14-OCT-2002 (first entry)

DE Human polypeptide SEQ ID NO 357.

KW Human; vulnery; dermatological; neuroprotective; neurotropic; cancer;
KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
KW burn; central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; immune disorder;
KW autoimmune disorder; multiple sclerosis; diabetes; allergy.

OS Homo sapiens.

XX WO200218424-A2.

XX PD 07-MAR-2002.

XX PF 31-AUG-2001; 2001WO-US027093.

XX PR 01-SEP-2000; 2000US-00654935.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

XX PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;

XX DR WPI; 2002-583321/62.

XX DR N-PSDB; ABQ93399.

XX PT New polynucleotide and polypeptides, useful for treatment and diagnosis
of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
sclerosis, diabetes and allergies.

XX PS Claim 20; SEQ ID NO 357; 284pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (I) comprising one of
245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
administering to a mammalian subject a composition comprising the protein
(II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
(I), (II) and (III) are useful for diagnostic evaluation of disorders.
(I) is useful for gene therapy of diseases and (II) can be used for

| | | | | | | |
|----|-----|------|-----|---|----------|-----------|
| 26 | 458 | 43.0 | 189 | 6 | ABO24960 | Human sec |
| 27 | 458 | 43.0 | 189 | 6 | ABU66965 | Human sec |
| 28 | 458 | 43.0 | 189 | 6 | ADA45759 | Novel hum |
| 29 | 458 | 43.0 | 189 | 6 | ADA76190 | Human PRO |
| 30 | 458 | 43.0 | 189 | 6 | ADA18840 | Human PRO |
| 31 | 458 | 43.0 | 189 | 6 | ADA61463 | Homo sapi |
| 32 | 458 | 43.0 | 189 | 6 | ADB19248 | Novel hum |
| 33 | 458 | 43.0 | 189 | 6 | ADP27789 | Human PRO |
| 34 | 458 | 43.0 | 189 | 6 | ADA86268 | Novel hum |
| 35 | 458 | 43.0 | 189 | 6 | ABD15832 | Human PRO |
| 36 | 458 | 43.0 | 189 | 6 | ADA47618 | Human PRO |
| 37 | 458 | 43.0 | 189 | 6 | ADA67413 | Human PRO |
| 38 | 458 | 43.0 | 189 | 6 | ADB30420 | Human PRO |
| 39 | 458 | 43.0 | 189 | 6 | ADA85716 | Novel hum |
| 40 | 458 | 43.0 | 189 | 6 | ADA96928 | Human PRO |
| 41 | 458 | 43.0 | 189 | 6 | ADA79232 | Human PRO |
| 42 | 458 | 43.0 | 189 | 6 | ADA87371 | Novel hum |
| 43 | 458 | 43.0 | 189 | 6 | ADB16573 | Human PRO |
| 44 | 458 | 43.0 | 189 | 6 | ADA91665 | Novel hum |
| 45 | 458 | 43.0 | 189 | 6 | ADB14728 | Human PRO |

CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 5; Length 194;
 Best Local Similarity 99.5%; Pred. No. 3.9e-107;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYDGLRHRLGSGFESVNSYFDSFLELLGK 60
 DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYDGLRHRLGSGFESVNSYFDSFLELLGK 60
 QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
 DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
 QY 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVENTVWTLGCRPFMNSQ 180
 DB 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVENTVWTLGCRPFMNSQ 180
 QY 181 RAACICAEKEEEL 194
 DB 181 RAACICAEKEEEL 194

RESULT 2
 ADA57403
 ID ADA57403 standard; protein; 194 AA.

AC ADA57403;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein #204.
 XX
 KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.
 XX
 OS Homo sapiens.
 XX
 PN WO2002102994-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002WO-US008278.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI
 PI WPI; 2003-167512/16.
 DR N-PSDB; ADA56510.
 DR
 XX New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory

PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.

PS Claim 13; SEQ ID NO 1596; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from manure biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders, and for
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: The sequence data for
 CC this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
 Best Local Similarity 100.0%; Pred. No. 3.9e-107;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYDGLRHRLGSGFESVNSYFDSFLELLGK 60
 DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYDGLRHRLGSGFESVNSYFDSFLELLGK 60
 QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
 DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
 QY 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVENTVWTLGCRPFMNSQ 180
 DB 121 TCGANKYRCDAKFRWCLXICSDLKRSIGFVSKVEACDSLVDVTVENTVWTLGCRPFMNSQ 180
 QY 181 RAACICAEKEEEL 194
 DB 181 RAACICAEKEEEL 194

RESULT 3
 ADA56921
 ID ADA56921 standard; protein; 194 AA.

XX ADA56921;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein #204.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;

inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
multiple sclerosis; ischaemic brain injury; Parkinson's disease;
Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
triple helix formation; antisense gene therapy; forensic biology.

Homo sapiens.

WO2002102994-A2.

27-DEC-2002.

19-MAR-2002; 2002WO-US008278.

21-MAR-2001; 2001US-0277340P.

19-JUL-2001; 2001US-0306171P.

13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI: 2003-167512/16.

N-PSDB; ADA56025.

New human secreted polypeptides and polynucleotides, useful for
diagnosing, treating or preventing e.g. immune disorders, inflammatory
conditions, respiratory disorders, cancers, CNS disorders, or
neurodegenerative disorders.

Claim 13; SEQ ID NO 1111; 1754pp; English.

The invention relates to 592 new human secreted polypeptides useful for
diagnosing, treating or preventing e.g. immune disorders, inflammatory
conditions, respiratory disorders, cancers, CNS disorders, or
neurodegenerative disorders, or polypeptides comprising an amino acid
sequence at least 95% identical to the new sequences. The polypeptides,
antibodies or antibody fragments that bind to the polypeptides, nucleic
acids encoding the polypeptides, agonists or antagonists that binds to
the polypeptide, are useful in preparing diagnostic or pharmaceutical
compositions for diagnosing, treating or preventing an e.g. immune
disorders, inflammatory conditions (e.g. inflammatory bowel disease,
nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
(e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
disorders (e.g. Parkinson's disease or Alzheimer's disease), and
cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
polynucleotides are useful for chromosome identification, chromosome
mapping, for controlling gene expression through triple helix formation
or antisense DNA or RNA, in gene therapy, for identifying individuals
from minute biological samples, in forensic biology, and as hybridization
probes. The polypeptides are useful for as molecular weight markers on
sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
gels, to raise antibodies, for testing biological activities, and for
treating or preventing neural disorders, immune system disorders,
muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
renal, proliferative and/or cancerous diseases. This sequence corresponds
to one of the polypeptide of the invention. Note: The sequence data for
this patent did form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
Best Local Similarity 99.5%; Pred. No. 3 9e-107;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLMISLGGGLAQSDTSPTESYSDWGLRHRLRGFSFVNSYFDSFLELLGK 60
DB 1 MKLASGFLVLMISLGGGLAQSDTSPTESYSDWGLRHRLRGFSFVNSYFDSFLELLGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKQPEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120

Db 61 NGVCQYRCRYGKAPMPRGYKQPEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXSIKSLKRSISLGFYSKVEACDSLDVDTVENTVWTLGCRPFMNSQ 180
Db 121 TCGANKYRCDAKFRWCLXSIKSLKRSISLGFYSKVEACDSLDVDTVENTVWTLGCRPFMNSQ 180
QY 181 RAACICAEKEEL 194
Db 181 RAACICAEKEEL 194

RESULT 4
ADA41278
ID ADA41278 standard; protein; 194 AA.
AC ADA41278;
XX 20-NOV-2003 (first entry)
XX Human secreted protein.
XX Human; secreted protein; cancer; hyperproliferative disorder;
XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
XX anaemia; allergic reaction; asthma; cardiovascular disorder;
XX wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
XX antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
XX vulnery; cardiant; gene therapy.
XX Homo sapiens.
XX WO2002102993-A2.
XX 27-DEC-2002.
XX 19-MAR-2002; 2002WO-US008123.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI: 2003-175238/17.
XX New human secreted proteins and nucleic acid molecules, useful for
XX preparing a diagnostic or pharmaceutical composition for diagnosing,
XX preventing or treating cancer or other hyperproliferative disorder,
XX asthma, allergies or AIDS.
XX Claim 1; SEQ ID NO 1661; 3205pp; English.
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX treating or ameliorating medical conditions e.g. by protein or gene
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX fragments, and agonists or antagonists that bind to the polypeptide are
XX useful for preparing a diagnostic or pharmaceutical composition for
XX diagnosing or treating cancer or other hyperproliferative disorder. The
XX polypeptides and nucleic acid molecules are also useful for detecting,
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX or other hyperproliferative disorders including neoplasms, autoimmune
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,
XX thrombocytopenia), allergic reactions including asthma or eczema,
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX fungal or viral infections including HIV/AIDS), or wound healing and
XX disorders of epithelial cell proliferation. The nucleic acids are also

CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.9e-107;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60
DB 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXSCDLKRSGLGFVSKVEACDLSLVDVTNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDAKFRWCLXSCDLKRSGLGFVSKVEACDLSLVDVTNTVTLGCRPFMNSQ 180
QY 181 RAACICAEKEEKEEL 194
DB 181 RAACICAEKEEKEEL 194

RESULT 5
ADA40769
ID ADA40769 standard; protein; 194 AA.
AC ADA40769;
DT 20-NOV-2003 (first entry)
XX Human secreted protein.
DE
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antitumoral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnary; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
FN WO2002102993-A2.
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1151; 3205pp; English.

XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
Best Local Similarity 99.5%; Pred. No. 3.9e-107;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60
DB 1 MKLASGFLVWLGLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXSCDLKRSGLGFVSKVEACDLSLVDVTNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDAKFRWCLXSCDLKRSGLGFVSKVEACDLSLVDVTNTVTLGCRPFMNSQ 180
QY 181 RAACICAEKEEKEEL 194
DB 181 RAACICAEKEEKEEL 194

RESULT 6
ABO13978
ID ABO13978 standard; protein; 194 AA.
XX
AC ABO13978;
XX
DT 21-AUG-2003 (first entry)
XX
DE Novel human secreted protein #7.
XX
KW Human; secreted protein; cytostatic; neuroprotective; hepatotropic;
KW gene therapy; cancer; liver disorder; hepatitis; neural disorder;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FN US2003028003-A1.
XX
PD 06-FEB-2003.
XX

PF 12-OCT-2001; 2001US-00974879.

XX 07-NOV-1997; 97US-0064900P.
PR 07-NOV-1997; 97US-0064908P.
PR 07-NOV-1997; 97US-0064911P.
PR 07-NOV-1997; 97US-0064912P.
PR 07-NOV-1997; 97US-0064983P.
PR 07-NOV-1997; 97US-0064984P.
PR 07-NOV-1997; 97US-0064985P.
PR 07-NOV-1997; 97US-0064987P.
PR 07-NOV-1997; 97US-0064988P.
PR 17-NOV-1997; 97US-0066083P.
PR 17-NOV-1997; 97US-0066090P.
PR 17-NOV-1997; 97US-0066094P.
PR 17-NOV-1997; 97US-0066095P.
PR 17-NOV-1997; 97US-0066100P.
PR 04-NOV-1998; 98WO-US023435.
PR 05-MAY-1999; 99US-00305736.
PR 13-OCT-2000; 2000US-0239893P.
PR 28-MAR-2001; 2001US-00818683.
XX (ROSE/) ROSEN C A.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJ/) NI J.
PA (WEI/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAF/) LAFLEUR D W.
PA (SHI/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
PA (BIRS/) BIRSE C E.
XX Rosen CA, Feng P, Ruben SM, Ebner R, Olsen HS, Ni J, Wei Y;
PI Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;
PI Endress GA, Carter KC, Birse CE;
XX WPI; 2003-479549/45.
DR N-PSDB; ACD18865.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer,
PT liver disorders such as hepatitis or neural disorders such as Alzheimer's
PT disease.
XX
PS Claim 11; Page 357; 496pp; English.

XX The invention describes a new isolated nucleic acid molecule comprising a
CC sequence having at least 95% identity with a sequence comprising: (a) a
CC polynucleotide (PN) fragment of a sequence comprising 420-3435 bp, or its
CC allelic variant; (b) a PN fragment of the cDNA sequence; (c) a PN
CC sequence encoding a polypeptide, or its fragment, domain, epitope or
CC species homologue; or (d) a PN that hybridises under stringent conditions
CC to any one of the sequences of (A)-(C). The nucleic acid is useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition e.g., cancer, liver disorders such as hepatitis or neural
CC disorders such as Alzheimer's disease. This is the amino acid sequence of
CC a novel human secreted protein
XX
SQ Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.9e-107;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASFLVWLISLGGGLAQSDTSPTEESYSDWGLRHRLRGSPESVNSYFDSFLELLGK 60
DB 1 MKLASFLVWLISLGGGLAQSDTSPTEESYSDWGLRHRLRGSPESVNSYFDSFLELLGK 60

QY 61 NGVCQYRCRYGKAPMPRPYKQPENGGSGYFLGLKVPESMDLGI PAMTKCCNQLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPYKQPENGGSGYFLGLKVPESMDLGI PAMTKCCNQLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXSCSLDKRSILGFSYKVEACDLSLVDVTVTNTVTLGCRPFPMNSQ 180
DB 121 TCGANKYRCDAKFRWCLXSCSLDKRSILGFSYKVEACDLSLVDVTVTNTVTLGCRPFPMNSQ 180
QY 181 RAACICAEKEEL 194
DB 181 RAACICAEKEEL 194

RESULT 7

ABR48024 ID ABR48024 standard; protein; 194 AA.

XX ABR48024;

XX 12-JUN-2003 (first entry)

XX Human secreted protein, SEQ ID 915.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnery; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.

XX Homo sapiens.

XX WO200295010-A2.

XX 28-NOV-2002.

XX 19-MAR-2002; 2002WO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.

PS Claim 13; SEQ ID NO 915; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47633-
ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in

CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ

Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.9e-107;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSEFVSNSYFDSFLELLGGK 60
Db 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSEFVSNSYFDSFLELLGGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120
Db 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180
Db 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180
QY 181 RAACICAEKEEKEEL 194
Db 181 RAACICAEKEEKEEL 194

RESULT 8

ABR47739
ID ABR47739 standard; protein; 194 AA.

AC ABR47739;

DT 12-JUN-2003 (first entry)

XX Human secreted protein, SEQ ID 630.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnery; antiinflammatory; nootropic; neuroprotective;
XX antiparkinsonian; gene therapy; human; cardiovascular disorder.

OS Homo sapiens.

FN WO200295010-A2.

XX 28-NOV-2002.

PF 19-MAR-2002; 2002WO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.

XX Claim 13; SEQ ID NO 630; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders, for
CC proliferative disorders and/or cancerous diseases and conditions, for

CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ

Sequence 194 AA;

Query Match 99.8%; Score 1064; DB 6; Length 194;
Best Local Similarity 99.5%; Pred. No. 3.9e-107;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSEFVSNSYFDSFLELLGGK 60
Db 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSEFVSNSYFDSFLELLGGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120
Db 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIKVPATKCCNOLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180
Db 121 TCGANKYRCDAKFRWCLXISCSDLKRSIGFVSKVEACDSLVDVTVTWTLGCRPFMNSQ 180
QY 181 RAACICAEKEEKEEL 194
Db 181 RAACICAEKEEKEEL 194

RESULT 9

AAAY27572
ID AAAY27572 standard; protein; 195 AA.

XX AAAY27572;

XX 30-JUL-1999 (first entry)

XX Human secreted protein encoded by gene No. 6.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX WO9924836-A1.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US023435.

XX 07-NOV-1997; 97US-0064900P.

PR 07-NOV-1997; 97US-0064908P.

PR 07-NOV-1997; 97US-0064911P.

PR 07-NOV-1997; 97US-0064983P.

PR 07-NOV-1997; 97US-0064984P.

PR 07-NOV-1997; 97US-0064985P.

PR 07-NOV-1997; 97US-0064987P.

PR 07-NOV-1997; 97US-0064988P.
 PR 17-NOV-1997; 97US-0066089P.
 PR 17-NOV-1997; 97US-0066090P.
 PR 17-NOV-1997; 97US-0066094P.
 PR 17-NOV-1997; 97US-0066095P.
 PR 17-NOV-1997; 97US-0066100P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Feng P, Carter KC, Endress GA, Rosen CA, Ruben SM, Janat F;
 PI Wei Y, Moore PA, Soppet DR, Kyaw H, Lafleur DW, Olsen HS;
 PI Shi Y, Ebner R;
 XX
 DR WPI; 1999-337740/28.
 DR N-PSDB; AAX84938.
 XX
 XX New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders.
 XX
 PS Claim 11; Page 352-353; 507pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAX84924) for increasing the stability of the fused protein
 CC as compared to the human protein only. The invention relates to 125 novel
 CC genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino
 CC acid sequences AA27567-Y27933) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 125 polynucleotides, based on which tissues they are most highly
 CC expressed in (see AAX84933 for described uses)
 XX
 SQ Sequence 195 AA;
 Query Match 99.8%; Score 1064; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 3.9e-107;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLASFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60
 DB 1 MKLASFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60
 QY 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
 DB 61 NGVCQYRCRYGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120
 QY 121 TCANKYRCDAKFRWCLXICSDLKRSGLGFVSKVEACDSLVDVTFVNTVMTLGRPFMNSQ 180
 DB 121 TCANKYRCDAKFRWCLXICSDLKRSGLGFVSKVEACDSLVDVTFVNTVMTLGRPFMNSQ 180
 QY 181 RAACICAEKEEL 194
 DB 181 RAACICAEKEEL 194
 RESULT 10
 ADE08422 ID ADE08422 standard; protein; 335 AA.
 XX AC ADE08422;
 XX AC ADE08422;
 XX AC ADE08422;
 DT 29-JAN-2004 (first entry)
 XX Novel protein (useful for identifying genetic disorders) #577.
 DE novel gene; novel protein; tissue marker; molecular weight marker;
 XX novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX

PN WO2003054152-A2.
 XX 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI; 2003-569235/53.
 DR N-PSDB; ADE07511.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1488; 1177pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 335 AA;
 Query Match 61.5%; Score 655.5; DB 7; Length 335;
 Best Local Similarity 60.5%; Pred. No. 1.9e-62;
 Matches 133; Conservative 6; Mismatches 16; Indels 65; Gaps 3;
 QY 1 MKLASFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60
 DB 1 MKLASFLVWLISLGGGLAQSDTSPDTEESYSDWGLRHRLGSPESVNSYFDSFLELLGGK 60
 QY 61 NGVCQYRCRYG-----KAPMPRGYKQEPNGCGSYF--LGLKVPE----- 99
 DB 61 NGVCQYRCRYGCAVSLSVKTVAGGPMDSPREVTICLALFPVHLPLDLADKNQNSIKR 120
 QY 100 -----SMDLGIPTAMTKCCNQL 115
 DB 121 LKQILVAEFLAGGSGSQQLGKKSKWFESHYSVTSSSSSPDLMDLGIPTAMTKCCNQL 180
 QY 116 DVCYDTCGANKYRCDAKFRWCLXICSDLKRSGLGFVSKVE 155
 DB 181 DVCYDTCGANKYRCDAKFRWCLXICSDLKRSGLGFVSKVE 220
 RESULT 11
 AAY88282 ID AAY88282 standard; protein; 192 AA.
 XX AC AAY88282;
 XX AC AAY88282;
 DT 16-OCT-2000 (first entry)
 XX Murine TANGO 180 protein.
 DE TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;
 XX

KW TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;
KW secreted protein; transmembrane protein; gene therapy; vaccine;
KW diagnosis; treatment; detection.
XX
OS Mus sp.
XX
PN WO200018904-A2.
XX
XX 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US022817.
XX
XX 30-SEP-1998; 98US-00164220.
PR 02-OCT-1998; 98US-00164169.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
PA Barnes TM;
PI
XX
XX WPI: 2000-293144/25.
DR N-PSDB; AAA39955, AAA39956.
DR
XX
XX Isolated nucleic acids encoding TANGO polypeptides useful for preventing,
PT diagnosing and treating diseases associated with inappropriate protein
PT expression.
XX
XX Claim 9; Fig 2; 249pp; English.
PS
XX This invention describes novel human and murine nucleic acids encoding
CC TANGO polypeptides (which are either wholly secreted or transmembrane
CC proteins) which can be used for gene therapy and/or vaccination. The
CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic
CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
CC polypeptides according to standard recombinant DNA methodologies. They
CC may also be used to detect and quantify the presence of TANGO nucleic
CC acids in a sample and therefore identify or diagnose diseases associated
CC with inappropriate TANGO expression (e.g. diseases related to over or
CC under expression of the polypeptides or the expression of inactive
CC polypeptides). The nucleic acids and the polypeptides they encode may be
CC used according to standard gene therapy protocols, to treat diseases
CC associated with inappropriate TANGO expression by supplementing a
CC patient's own production of the polypeptide or to rectify mutations that
CC may result in expression of an abnormally active polypeptide. The
CC polypeptides may also be used to identify and produce agonists and
CC antagonists of TANGO expression and activity which may be used to
CC modulate TANGO related processes and diseases. The polypeptides are
CC particularly useful for use as antigens for producing antibodies to TANGO
CC proteins which may be used for inhibiting the activity of TANGO proteins.
CC They may also be used to detect and quantify the presence of TANGO
CC proteins in samples and therefore identify patients in whom the protein
CC is over- or under-expressed. This sequence represents the murine TANGO
CC 180 protein described in the method of the invention
XX
XX Query Match 43.8%; Score 467; DB 3; Length 192;
XX Best Local Similarity 43.9%; Pred. No. 2.9e-42;
XX Matches 83; Conservative 43; Mismatches 49; Indels 14; Gaps 3;
QY 8 LVLWLSLGGGLAQSDTSPTDESYSW-GLRHLSGFESVNSYFSLFLGGKNGVQ 65
DB 16 LLLLTATARGQDQQT-----TDWRTLKTIRNGHKITLYNAAALLGGEDGLQ 67
QY 66 YRCYKAPMPRGYKPPQPNCGGCVFLGLKVPESMDLGI PAMTKCNOLDVCYDFCGAN 125
DB 68 YKSDGSKVPVRYGYPSPNGCGSPFLGV-----HLNIGIPSLTKCNQHDRCYETCGKS 123
QY 126 KYRCDAKFRWCLXISCDLKRISGFYSKVEACDLSLDTVNTWTLGCRPFMNSQRAACI 185
DB 124 KNDCEEFQYCLSKICRDVQKTLGLSQNVQACETTVELLFDPSVHLGCKPFLDYSRAACW 183
QY 186 CAEEKEEL 194
| | | | |

DB 184 CRYEEKTDL 192
RESULT 12
ABB08151
ID ABB08151 standard; protein; 192 AA.
XX
XX ABB08151;
AC
XX 10-SEP-2002 (first entry)
DT
XX Murine GXII PLA2 (mGXII-1 PLA2) polypeptide.
DE
XX Phospholipase A2; GXII PLA2; phosphatidylethanolamine; Th2; GV PLA2;
KW transgenic; immunosuppressive; antiallergic; cytostatic; antimicrobial;
KW antidiabetic; antirheumatic; antiarthritic; antiinflammatory; mouse;
KW neuroprotective; cerebroprotective; antiinfertility; contraceptive;
KW mGXII-1 PLA2; enzyme.
XX
XX Mus musculus.
OS
XX WO200240655-A2.
PN
XX 23-MAY-2002.
PD
XX 06-NOV-2001; 2001WO-US044125.
PF
XX 06-NOV-2000; 2000US-0246316P.
PR
XX (HARD) HARVARD COLLEGE.
XX
XX Ho I, Arm JP, Austen KF, Glimcher LH;
PI
XX WPI: 2002-500219/53.
DR N-PSDB; ABL60856.
XX
XX New group XII phospholipase A2 protein, useful for identifying modulators
PT used for modulating prostaglandin production by Th2 cell and Th2 cell
PT differentiation/activity, and treating allergy, cancer and type I
PT diabetes.
XX
XX Claim 17; Page 73-74; 77pp; English.
PS
XX The invention relates to an isolated group XII phospholipase A2 (GXII
CC PLA2) protein or its biologically active portion, where the protein
CC selectively hydrolyses arachidonic acid in sn-2 position of
CC phosphatidylethanolamine. Methods of modulating Th2 cell differentiation
CC activity by modulating either GXII PLA2 or GV PLA2 which is also
CC preferentially expressed in T cells are provided. The GXII PLA2 proteins
CC can be used to prepare anti-GXII PLA2 antibodies. The GXII PLA2 encoding
CC nucleic acid molecules can be used to prepare non-human transgenic
CC animals that contain cells carrying a transgene encoding GXII PLA2
CC protein or a portion of GXII PLA2 protein. Prostaglandin production can
CC be increased by stimulators of GXII PLA2 or GV PLA2 which is further
CC useful for prolonging survival of the graft and thus has applications in
CC bone marrow transplantation or solid organ transplantation, and for
CC increasing production of Th2-promoting cytokines for commercial purposes.
CC Modulating the type of T helper cell response mounted in the individual
CC suffering from the disease condition e.g., inhibition of Th2 cell
CC response using GXII PLA2 or GV PLA2 inhibitors is carried out for
CC inhibiting prostaglandin production to thereby inhibit production of Th2-
CC associated cytokines in: (a) allergic patients to downregulate production
CC of pathogenic IGE antibodies; (b) cancer patients; and (c) subjects with
CC infectious diseases. Stimulation of Th2 cell response using GXII PLA2 or
CC GV PLA2 stimulators is useful for treating autoimmune diseases associated
CC with Th2-type dysfunction, such as type I diabetes, rheumatoid arthritis,
CC etc. The methods provided are also useful in treating conditions such as
CC inflammation, arthritis, multiple sclerosis, stroke, infertility, and
CC also have contraceptive uses. The present sequence represents the mouse
CC GXII PLA2 (mGXII-1 PLA2)
XX
XX Sequence 192 AA;

Sequence 189 AA; SQ

| | | | | |
|-----------------------|--------------|--------------------|----------------|-------------|
| Query Match | 43.0% | Score 458; | DB 3; | Length 189; |
| Best Local Similarity | 43.4%; | Pred. No. 2.7e-41; | | |
| Matches 82; | Conservative | 42; | Mismatches 55; | Indels 10; |
| | | | | Gaps 3; |

| | | | |
|----|---|---|----|
| Qy | 8 | LVLWLSGGGGLAQSDTSPDTEESYSDW-GLRHRLRGFSFVSNSYFDSFLELLGGNGVCQ | 65 |
| Dh | 9 | LTLLIIIMAAVVRCEQCAOT---TDWRATLKTIRNGVHKIDYLNAAALDGLGEDGLCQ | 64 |

QY 66 YRCRYGKAPMPRPQYKPPQEPNGCGSYFLGLKVPESMDLGI PAMTKCCNQLDVCYDTCGAN 125

[illegible]

DB 65 YKCS DGS R P F F R Y G Y K P S P F P N G C S P L F G V - - - - H L N I G I P S L I A C C N Q H D R C I E I C G N S 120

QY 126 KYRCDAKFRWCLXSI CSDLKRS LGFVSKVEACDSLVDTVFNTVWTLGCRPFMNSQRAACI 185

Db 121 KNCDEEFOYCLSKI CRDVOQTGLTQHVCATTVELLFDSVIHLGCKPYLDSQRAACR 180

ON 186 CAFEKEET, 194

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| 94 | — |
| 95 | — |
| 96 | — |
| 97 | — |
| 98 | — |
| 99 | — |
| 100 | — |

Db 181 CHYEKTDL 189

RESULT 14

AAV8/282
ID AAV87282 standard: protein; 189 AA.

XX
XX

AC
AY87282;
VV

DT 11-MAY-2000 (first entry)

XX

DE Human signal peptide containing protein HSPF-39 SEQ ID NO:39.
XX

Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW

KW inflammation, cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antitumour; gene therapy; cell proliferation; neurological disorder;
KW autoimmune disease; developmental disorder; arteriosclerosis;
KW reproductive disorder; acquired immune deficiency syndrome; anaemia;
KW cirrhosis; psoriasis; infection; Alzheimer's disease; schizophrenia;
KW asthma; Crohn's disease; Huntington's diseases; ovulatory defect;
KW Parkinson's disease; muscular dystrophy.

xx
OS
Homo sapiens.
xx

PN WO30000610-A2.
XX
PD 06-JAN-2000.

XX
PF 25-JUN-1999; 99NO-US014484.

| | | |
|----|--------------|-----------------|
| XX | 26-JUN-1998; | 98US-0090762P. |
| PR | 21 JUL 1998. | 0811S-00041997P |

| | | |
|----|--------------|----------------|
| PR | 01-OCT-1998; | 98US-0102686P. |
| PR | 11-DEC-1998; | 98US-0112129P. |
| PR | 31-OCT-1998; | 98US-0034365P. |

XX
PA {INCY-} INCYTE PHARM INC.

XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;

```
XX WPI; 2000-160673/14.
DR N-PSDB; AAZ98167.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
XX disease.
XX
XX Claim 1; Page 201; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AY87224 to AY87357 which represent the
XX human signal peptide-containing proteins HSPF-1 to HSPF-134. HSPFs have
XX anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
XX neuroprotective, cardiovascular and antiaesthetic activities, and can be
XX used in gene therapy. HSPFs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSPF. Antagonists of
XX HSPF are used to treat or prevent disorders associated with increased
XX activity or function of HSPF. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPF
XX nucleic acids can be used for the recombinant production of HSPF, for
XX detecting HSPF in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
XX or ribozyme therapeutics, for detecting related sequences or genetic
XX variations, and for chromosomal mapping. HSPF are also used to raise
XX specific antibodies (Ab) and to screen for agonists and antagonists
XX (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPF
XX -related diseases (in usual immunoassays), as therapeutic antagonists, in
XX competitive drug screens, and for purification of HSPF from natural
XX sources
XX
XX Sequence 189 AA;
XX
XX Query Match 43.0%; Score 459; DB 3; Length 189;
XX Best Local Similarity 43.4%; Pred. No. 2.7e-41;
XX Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;
XX
QY 8 LVMLSLGGLAQSDTSPTEESYSDW--GLHRLGRSFESVNSYFDSFLLELGGKNGVCQ 65
DB 9 LTLILLMAAVRVCBOQAQT---TDWRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCYRKAMPMPRGYPQPNCGSYFLGLKVPESMDLGPAMTKCCNOLDVCYDTCCGAN 125
DB 65 YKCSGSKFPPRYGYKPPNGCGSPLFGV---HLNIGIPSLTKCCNHDRCYETCGKS 120
QY 126 KYRCDAKFWCLXSCSLDKRSLGFSKVEACDSLVDTVFNVTWTLGCRPPFNWSQRAACI 185
DB 121 KNDCEBEFYCLSKICRDYQKTLGLTQHVQACETTVLELFDLSVIHLGCKPYLDSPRAACR 180
QY 186 CAEEKEEL 194
DB 181 CHYEKTDL 189
XX
XX RESULT 15
XX AAE06607
XX ID AAE06607 standard; protein; 189 AA.
XX
XX AAE06607;
XX
XX 25-SEP-2001 (first entry)
XX
XX Human protein having hydrophobic domain, HP10797.
XX
XX Human; hydrophobic domain; gene therapy; nutritional supplement;
XX cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
XX multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
XX haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
XX Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
```

```
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
XX contraceptive; antiinfertility; antiinflammatory.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein 24..189
XX /note= "Mature human protein with hydrophobic domain"
XX
XX WO200149728-A2.
XX
XX 12-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-JP009359.
XX
XX 06-JAN-2000; 2000JP-00000585.
XX 06-JAN-2000; 2000JP-00000588.
XX 11-JAN-2000; 2000JP-00002299.
XX 03-FEB-2000; 2000JP-00026862.
XX 03-MAR-2000; 2000JP-00058367.
XX
XX (PROT-) PROTEGENE INC.
XX (SAGA) SAGAMI CHEM RES CENT.
XX
XX Kato S, Kimura T;
XX
XX WPI; 2001-418355/44.
XX N-PSDB; AAD12602.
XX
XX Human proteins with hydrophobic domains and the nucleic acids encoding
XX them, useful for preventing diagnosing and treating e.g. cancer,
XX Alzheimer's and inflammation.
XX
XX Claim 1; Page 443-444; 563pp; English.
XX
XX The present sequence is human protein with hydrophobic domain, HP10797.
XX The polynucleotide and polypeptide of the invention may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate polypeptide expression. The polynucleotides may be used to
XX produce the polypeptide, by inserting the nucleic acids into a host cell
XX and culturing the cell to express the protein. The polynucleotides and
XX its complementary sequences may also be used as DNA probes in diagnostic
XX assays and also used in gene therapy. The polypeptides may also be used
XX as antigens in the production of antibodies and in assays to identify
XX modulators of polypeptide expression and activity. The polypeptides and
XX nucleic acids may be used as nutritional supplements, to modulate
XX cytokine and cell proliferation activity, to modulate immune stimulation
XX or suppression (e.g. for the treatment of microbial infections and
XX autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and
XX insulin-dependent diabetes), to modulate haematopoiesis, to modulate
XX tissue growth activity (e.g. for the treatment of Parkinson's disease,
XX Huntington's disease and Alzheimer's disease), to modulate activin and
XX inhibin activity (e.g. for controlling fertility), to modulate
XX chemotactic and chemokinetic activity, to modulate haemostatic and
XX thrombolytic activity, to modulate receptor ligand activity, to modulate
XX inflammation and to inhibit tumour growth
XX
XX Sequence 189 AA;
XX
XX Query Match 43.0%; Score 459; DB 4; Length 189;
XX Best Local Similarity 43.4%; Pred. No. 2.7e-41;
XX Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;
XX
QY 8 LVMLSLGGLAQSDTSPTEESYSDW--GLHRLGRSFESVNSYFDSFLLELGGKNGVCQ 65
DB 9 LTLILLMAAVRVCBOQAQT---TDWRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCYRKAMPMPRGYPQPNCGSYFLGLKVPESMDLGPAMTKCCNOLDVCYDTCCGAN 125
DB 65 YKCSGSKFPPRYGYKPPNGCGSPLFGV---HLNIGIPSLTKCCNHDRCYETCGKS 120
```


QY 126 KYRCDKFRWCLXSICSDLKRSIGFVSKVEACDSLVDVTVENTVTWTLGCRPFMNSQRAACI 185
Db 121 KNDCEBEPQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQRAACR 180
QY 186 CAERKEEL 194
Db 181 CHYEKTDL 189

Search completed: May 17, 2004, 10:42:16
Job time : 62 secs


```

;
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-175

Query Match      34.4%; Score 367; DB 4; Length 123;
Best Local Similarity 50.0%; Pred. No. 2.6e-34;
Matches 62; Conservative 27; Mismatches 31; Indels 4; Gaps 1;

QY 71 GKAMPBPGYKQBPNGGSGYFLGLKVPESMDLGPAMTKCCNOLDVCYDTCGANKYRCD 130
DB 4 GSKPPFRVGYKPSPPNGGSGFLGV-----HUNIGIPSLTKCCNQHDRCYETCGKSKNDCD 59
QY 131 AKFRWLXISICSLKRSIGFVSKVEACDSLVDTVNTVMTLGCRRPFMNSQRAACICAE 190
DB 60 EEFQYCLSKICRDVQKTLGLTQHVOACETTVELLFDVSVHLGCKPYLDSQRAACRCHYEE 119
QY 191 KEEL 194
DB 120 KTDL 123

RESULT 4
US-08-485-449-6
; Sequence 6, Application US/08485449
; Patent No. 5824789
; GENERAL INFORMATION:
; APPLICANT: VANDENBERG, DAVID
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,449
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKE, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20296-20035.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-449-6

Query Match      7.9%; Score 84.5; DB 2; Length 389;
Best Local Similarity 22.0%; Pred. No. 0.27;
Matches 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5;

QY 59 GKNVGCYQRYCKAPMPR-----PGYKQBPNGGSGY 91
DB 251 GTSGSQFKTCWBAAPFEAIGAALRAERLSRAIFIDTHNRNSGAFQPLRLPRLSGLVY 310
QY 92 FLGLKVPESMD-----LGIPAMT-KCCNOLDVCYDTCGA-----NKYRCDAKF 133
```

Db 311 F--EKSPDFCERDPTLGSPTGRACNKTSLRLLDGGSLCCGRGHNVLRQTRVERCHCRF 368
QY 134 RWCLXSICDLK 145
Db 369 HWCYVLCDECK 380

RESULT 5
US-08-833-963C-2
; Sequence 2, Application US/08833963C
; Patent No. 5916769
; GENERAL INFORMATION:
; APPLICANT: Olsen, et al.
; TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
; TITLE OF INVENTION: HCA858X
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,963C
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/05033
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PP258
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-963C-2

Query Match 7.8%; Score 83.5; DB 2; Length 443;
Best Local Similarity 21.8%; Pred. No. 0.42;
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;
QY 6 GFLVLW----LSLGGGLAQSPTSPTDEESYSD---W--GLRHRL-----GSP 43
Db 10 GSLLLWALLLLGLSASPDSEEDSYCTDGYEWDPSQCHRDVNECLTIPEACKGEM 69
QY 44 ESNVSYFDSFLELLGGKNGVCQYRC-----RYGKAMP-----RPGYKP 82
Db 70 KCINHY-----GG-----YLCLPSAAVINDLHGEPPPPVPPAQAHPNCPGYP 115
QY 83 QEPNGCGSYFLGLKVPESMDLGIPTAMTKC-----CNQLDVCYDTGANKYR-----C--- 129
Db 116 DDQSC-----VDVDECAQALHDCRPSQCHNLPGSYQCTCPGYRKIGPECVDI 165
QY 130 -DAKFRWCLXSICDLKSL-----GF-----VSKVEACD---SLVDTVFNVTWL 171
Db 166 DECRYRYCOHR-CVNLPGSFRQCQEPGFLGNPNRSCVDVNECDMGAPCEQRCFNSYGT 224
QY 172 GCR 174
|||

Db 225 LCR 227

RESULT 6
US-08-980-514-1
; Sequence 1, Application US/08980514
; Patent No. 6004753
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT
; TITLE OF INVENTION: EIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,514
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0436 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT13
; CLONE: 2786449
; US-08-980-514-1

Query Match 7.8%; Score 83.5; DB 3; Length 443;
Best Local Similarity 21.8%; Pred. No. 0.42;
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;
QY 6 GFLVLW----LSLGGGLAQSPTSPTDEESYSD---W--GLRHRL-----GSP 43
Db 10 GSLLLWALLLLGLSASPDSEEDSYCTDGYEWDPSQCHRDVNECLTIPEACKGEM 69
QY 44 ESNVSYFDSFLELLGGKNGVCQYRC-----RYGKAMP-----RPGYKP 82
Db 70 KCINHY-----GG-----YLCLPSAAVINDLHGEPPPPVPPAQAHPNCPGYP 115
QY 83 QEPNGCGSYFLGLKVPESMDLGIPTAMTKC-----CNQLDVCYDTGANKYR-----C--- 129
Db 116 DDQSC-----VDVDECAQALHDCRPSQCHNLPGSYQCTCPGYRKIGPECVDI 165
QY 130 -DAKFRWCLXSICDLKSL-----GF-----VSKVEACD---SLVDTVFNVTWL 171
Db 166 DECRYRYCOHR-CVNLPGSFRQCQEPGFLGNPNRSCVDVNECDMGAPCEQRCFNSYGT 224
QY 172 GCR 174
|||

RESULT 7

US-08-485-449-2
; Sequence 2, Application US/08485449
; Patent No. 5824789

GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20296-20035.00
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 389 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-449-2

Query Match 7.7%; Score 82.5; DB 2; Length 389;

Best Local Similarity 21.2%; Pred. No. 0.46;

Matches 28; Conservative 16; Mismatches 41; Indels 47; Gaps 5;

QY 59 GKNGVCQYRCRYGKAPMPR-----PGYKQEPNCGGSY 91

Db 251 GTSGSCQKFCWCRAAEFRAVGAALRRLGRLAIFDTHNRNSGAFQPLRPRLSGELVY 310

QY 92 FLGLKVPESMD----LGIPAMT-KCCNQLDVCYDTGCA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTMGSPGTRGRACNKTSLRLDGGSLCCGRGHNVLRQTRVERCHCRF 368

QY 134 RWCLXSICSLDK 145

Db 369 HWCYVLCDECK 380

RESULT 8

US-08-485-449-7

; Sequence 7, Application US/08485449

; Patent No. 5824789

GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID

TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,449

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.

REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 20296-20035.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 389 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-485-449-7

Query Match

Best Local Similarity 21.2%; Score 82.5; DB 2; Length 389;

Matches 28; Conservative 16; Mismatches 41; Indels 47; Gaps 5;

QY 59 GKNGVCQYRCRYGKAPMPR-----PGYKQEPNCGGSY 91

Db 251 GTSGSCQKFCWCRAAEFRAVGAALRRLGRLAIFDTHNRNSGAFQPLRPRLSGELVY 310

QY 92 FLGLKVPESMD----LGIPAMT-KCCNQLDVCYDTGCA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTMGSPGTRGRACNKTSLRLDGGSLCCGRGHNVLRQTRVERCHCRF 368

QY 134 RWCLXSICSLDK 145

Db 369 HWCYVLCDECK 380

RESULT 9

US-08-485-449-5

; Sequence 5, Application US/08485449

; Patent No. 5824789

GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID

TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,449

FILING DATE:

CLASSIFICATION: 536

```

; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20296-20035.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-449-5

Query Match 7.6%; Score 81; DB 2; Length 376;
Best Local Similarity 21.7%; Pred. No. 0.66;
Matches 28; Conservative 15; Mismatches 42; Indels 44; Gaps 5;

QY 59 GKNGVCVRCYRGKAPMR-----PGYKQPEPNCGGSYFL 93
Db 241 GTSGCGFKTCWRAAPFRAGAAERLRLAIFITHNNSGAFQRLRPRLSELVYF- 299
QY 94 GLKVPESMD---LGIPAMT-KCCNQLDVCYDTGCA-----NKYRCDAPKFWC 136
Db 300 -EKSPDFCFERDPTGSPGTRGRACNKTSLKLLDGGSLCCGRGHNVLRQTRVRCRCHCFHWC 358
QY 137 LXSICSLDK 145
Db 359 CYVLCDECK 367

RESULT 10
US-09-482-273-201
; Sequence 201, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 201
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-482-273-201

Query Match 7.4%; Score 79; DB 4; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.018;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 108 MTKCCNQLDVCYDTGCG 123
Db 1 LTKCCNQHDRCYETCG 16

RESULT 11
US-09-252-991A-21977
; Sequence 21977, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21977
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21977

Query Match 7.4%; Score 79; DB 4; Length 219;
Best Local Similarity 26.1%; Pred. No. 0.55;
Matches 30; Conservative 13; Mismatches 44; Indels 28; Gaps 5;

QY 67 RCRYGKAPMRPGYKQPEPNCGGSYFLG-----LKVPEMDLG 104
Db 10 RSRPSWAPWPKPG--AEKPMGCWREFFGRSADRGRYFKGEBILACHEAGITVFEKLTSG 67
QY 105 IPAMTKCCNQLDVCYDTGANKYRCDAA--KFRWCLXISCDLKSGLGFSVKVEAC 157
Db 68 ATAAGR-FGKGDFIYD-AAXNEYRCAPQSLIWRFSVEKGLKLRVWSSHCOGC 120

RESULT 12
US-08-185-432-16
; Sequence 16, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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US-08-185-432-16

Query Match 7.3%; Score 77.5; DB 1; Length 2471;
Best Local Similarity 23.6%; Pred. No. 19;
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;

QY 63 VCOY-----RCRYGKAPMPRP-GYKPOEPNGCGSYFLGLKVPESMDL-----103
DB 528 VCQIDIDDCSSTPCNLGAKCIDHPNGYEQ-----CATGFTGVLCENIDNCDPDPCHHGQ 583

QY 104 ---GIPAMTKCCN-----QLDVCYDTGANKYRC-----129
DB 584 CQGDIDSYTCICNPGYMGALCSQIDECYSSPCNLNDRGICIDLNVGYQCNCQPGTSGVNCE 643

QY 130 ----DAKFRWCLXSICSD-LKR-----SLGFVSKVEACDSLDVTFVNTVTLG--CRPFM 177
DB 644 INFDDCASNFCIHGICMDGINRYSCVSPGFTG--QRCNIDIDECASNPCRKGATCINGV 701

QY 178 NSORAACICAE 188
DB 702 NGFR--CICPE 710

RESULT 13

US-08-083-590A-19
; Sequence 19, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083.590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19

Query Match 7.3%; Score 77.5; DB 1; Length 2471;
Best Local Similarity 23.6%; Pred. No. 19;
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;

QY 63 VCOY-----RCRYGKAPMPRP-GYKPOEPNGCGSYFLGLKVPESMDL-----103
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QY 104 ---GIPAMTKCCN-----QLDVCYDTGANKYRC-----129
DB 584 CQGDIDSYTCICNPGYMGALCSQIDECYSSPCNLNDRGICIDLNVGYQCNCQPGTSGVNCE 643

QY 130 ----DAKFRWCLXSICSD-LKR-----SLGFVSKVEACDSLDVTFVNTVTLG--CRPFM 177
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QY 178 NSORAACICAE 188
DB 702 NGFR--CICPE 710

RESULT 14

US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-19

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Best Local Similarity 23.6%; Pred. No. 19;
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;

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QY 104 ---GIPAMTKCCN-----QLDVCYDTGANKYRC-----129
DB 584 CQGDIDSYTCICNPGYMGALCSQIDECYSSPCNLNDRGICIDLNVGYQCNCQPGTSGVNCE 643

QY 130 ----DAKFRWCLXSICSD-LKR-----SLGFVSKVEACDSLDVTFVNTVTLG--CRPFM 177

Db 644 INFDDCASNPCIHGICWDGINRYSCVSPGFTG--QRCNIDIDECASNPCRKGATCINGV 701
Qy 178 NSQRAACTICAE 188
Db 702 NGFR--CICPE 710

RESULT 15
US-08-899-232-1
; Sequence 1, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1

Query Match 7.3%; Score 77.5; DB 4; Length 2471;
Best Local Similarity 23.6%; Pred. No. 19;
Matches 45; Conservative 16; Mismatches 57; Indels 73; Gaps 11;
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Db 528 VCQIDIDDSCSTPCLNGAKCIDHENGVEQ---CATGFTGVLCENIDNCDDPDCHHGQ 583
Qy 104 ---GIPAMTKCCN-----QLDVCTCGANKYRC----- 129
Db 584 CQDGIDSYTCICNPGYMGAIQSDIDECYSFPCINDGRCIDLNVGYQCNCQFGTSGYNCE 643
Qy 130 ----DAKFERCLXSICSD-LKR----SLGFVSKVEACDSLVDTVFNTVTLG--CRPFM 177
Db 644 INFDDCASNPCIHGICWDGINRYSCVSPGFTG--QRCNIDIDECASNPCRKGATCINGV 701
Qy 178 NSQRAACTICAE 188
Db 702 NGFR--CICPE 710

Search completed: May 17, 2004, 10:48:07
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:43:49 ; Search time 46 Seconds
(without alignments)
1173.537 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLASGFLVLSLGGGLAQ.....PFMSQRAACIAEBEKEEL 194

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Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | ID | Description |
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| 1 | 1064 | 99.8 | 194 | 10 | US-09-974-879-145 |
| 2 | 1064 | 99.8 | 194 | 12 | US-10-621-401-145 |
| 3 | 1064 | 99.8 | 194 | 12 | US-10-363-616-357 |
| 4 | 1064 | 99.8 | 195 | 10 | US-09-305-736-144 |
| 5 | 1064 | 99.8 | 195 | 11 | US-09-818-683-144 |
| 6 | 467 | 43.8 | 192 | 9 | US-09-993-999-4 |
| 7 | 460.5 | 43.2 | 194 | 9 | US-09-975-374A-13 |
| 8 | 459 | 43.1 | 182 | 9 | US-09-975-374A-10 |
| 9 | 458 | 43.0 | 189 | 9 | US-09-867-550-1504 |
| 10 | 458 | 43.0 | 189 | 9 | US-09-993-999-2 |
| 11 | 458 | 43.0 | 189 | 9 | US-09-975-374A-2 |
| 12 | 458 | 43.0 | 189 | 12 | US-10-147-493-240 |
| 13 | 458 | 43.0 | 189 | 12 | US-10-145-127-240 |
| 14 | 458 | 43.0 | 189 | 12 | US-10-160-503-240 |
| 15 | 458 | 43.0 | 189 | 12 | US-10-169-395-97 |

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| 16 | 458 | 43.0 | 189 | 12 | US-10-143-118-240 |
| 17 | 458 | 43.0 | 189 | 12 | US-10-144-993-240 |
| 18 | 458 | 43.0 | 189 | 12 | US-10-158-787-240 |
| 19 | 458 | 43.0 | 189 | 12 | US-10-140-024-240 |
| 20 | 458 | 43.0 | 189 | 12 | US-10-140-808-240 |
| 21 | 458 | 43.0 | 189 | 12 | US-10-152-405-240 |
| 22 | 458 | 43.0 | 189 | 12 | US-10-127-852A-240 |
| 23 | 458 | 43.0 | 189 | 12 | US-10-127-900A-240 |
| 24 | 458 | 43.0 | 189 | 12 | US-10-128-685A-240 |
| 25 | 458 | 43.0 | 189 | 12 | US-10-131-820A-240 |
| 26 | 458 | 43.0 | 189 | 12 | US-10-142-886-240 |
| 27 | 458 | 43.0 | 189 | 12 | US-10-146-728-240 |
| 28 | 458 | 43.0 | 189 | 12 | US-10-146-786-240 |
| 29 | 458 | 43.0 | 189 | 12 | US-10-147-499-240 |
| 30 | 458 | 43.0 | 189 | 12 | US-10-157-798-240 |
| 31 | 458 | 43.0 | 189 | 14 | US-10-028-072-240 |
| 32 | 458 | 43.0 | 189 | 14 | US-10-121-043-240 |
| 33 | 458 | 43.0 | 189 | 14 | US-10-123-904-240 |
| 34 | 458 | 43.0 | 189 | 14 | US-10-140-474-240 |
| 35 | 458 | 43.0 | 189 | 14 | US-10-175-746-240 |
| 36 | 458 | 43.0 | 189 | 14 | US-10-176-918-240 |
| 37 | 458 | 43.0 | 189 | 14 | US-10-176-921-240 |
| 38 | 458 | 43.0 | 189 | 14 | US-10-137-865-240 |
| 39 | 458 | 43.0 | 189 | 14 | US-10-140-474-240 |
| 40 | 458 | 43.0 | 189 | 14 | US-10-142-431-240 |
| 41 | 458 | 43.0 | 189 | 14 | US-10-143-114-240 |
| 42 | 458 | 43.0 | 189 | 14 | US-10-140-003-240 |
| 43 | 458 | 43.0 | 189 | 14 | US-10-142-419-240 |
| 44 | 458 | 43.0 | 189 | 14 | US-10-123-262-240 |
| 45 | 458 | 43.0 | 189 | 14 | US-10-142-423-240 |

ALIGNMENTS

RESULT 1

US-09-974-879-145
; Sequence 145, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US 60/239,893
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17

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; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-974-879-145

Query Match          99.8%; Score 1064; DB 10; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-108;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120

QY 121 TCGANKYRCDAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180

QY 181 RAACICAEKEEKEEL 194
DB 181 RAACICAEKEEKEEL 194

RESULT 2
US-10-621-401-145
; Sequence 145, Application US/10621401
; Publication No. US20040038277A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2C1
; CURRENT APPLICATION NUMBER: US/10/621,401
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/974,879
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 611
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-621-401-145

Query Match          99.8%; Score 1064; DB 12; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-108;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120

QY 121 TCGANKYRCDAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180

QY 181 RAACICAEKEEKEEL 194
DB 181 RAACICAEKEEKEEL 194

RESULT 3
US-10-363-616-357
; Sequence 357, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-357

Query Match          99.8%; Score 1064; DB 12; Length 194;
Best Local Similarity 99.5%; Pred. No. 1.7e-108;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLWLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRPGYKQEPNGCGSYFLGLKVPESMDLGIIPAMTKCCNOLDVCYD 120

QY 121 TCGANKYRCDAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180
DB 121 TCGANKYRCDAKFRWCLXSCSLDKRSLGFVSKVEACDSLVDVTFTVNTVTLGCRPFMNSQ 180

QY 181 RAACICAEKEEKEEL 194
DB 181 RAACICAEKEEKEEL 194
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RESULT 4

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US-09-305-736-144
; Sequence 144, Application US/09305736
; Publication No. US2003008078A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: PZ020P1
; CURRENT APPLICATION NUMBER: US/09/305,736
; EARLIER FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
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; EARLIER APPLICATION NUMBER: 60/064,988
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; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 144
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (138)
; FEATURE:
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;
; Query Match          99.8%; Score 1064; DB 10; Length 195;
; Best Local Similarity 100.0%; Pred. No. 1.7e-108;
; Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy      1  MKLASGLVWLISLGGLAQSDTSPDTERSYSDWGLRHRLRGSFESVNSYFDSFLELLGGK 60
Db      1  MKLASGLVWLISLGGLAQSDTSPDTERSYSDWGLRHRLRGSFESVNSYFDSFLELLGGK 60
Qy      61  NGVCQYRCRYGKAPMPRPGYKPEPNGCGSYFLGLKVPSMDLIGIPAMTKCCNQLDVCDV 120
Db      61  NGVCQYRCRYGKAPMPRPGYKPEPNGCGSYFLGLKVPSMDLIGIPAMTKCCNQLDVCDV 120
Qy      121  TCGANKYRCDAKFRWCIXSCDLKRSLGFVSKEACDSLVDVTFTVNTLGCRRPFMNSQ 180
Db      121  TCGANKYRCDAKFRWCIXSCDLKRSLGFVSKEACDSLVDVTFTVNTLGCRRPFMNSQ 180
Qy      181  RAACICAEKEEL 194
Db      181  RAACICAEKEEL 194
;
; RESULT 6
; US-09-933-999-4
; Sequence 4, Application US/09993999
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: Ho, I-Cheng
; APPLICANT: Arm, Jonathan P.
; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; FILE REFERENCE: HUI-046
; CURRENT APPLICATION NUMBER: US/09/993,999
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,316
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Mus musculus

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Db 65 YKSDGSKPFRYGYKPSPPNGCGSPLFGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFVSKVEACDSLDVTFVNTVTLGCRPFMNSORAAI 185
Db 121 KNCDEEFQYCLSKICRDVQKTLGTHQVQACETTVELLFDVSVIHLGCKPYLDSORAAI 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 10
US-09-993-999-2
; Sequence 2, Application US/09993999
; Patent No. US20020110891A1
; GENERAL INFORMATION:
; APPLICANT: Ho, I-Cheng
; APPLICANT: Arm, Jonathan P.
; APPLICANT: Austen, K. Frank
; APPLICANT: Glimcher, Laurie H.
; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
; TITLE OF INVENTION: Expressed in Th2 Cells
; FILE REFERENCE: HUI-046
; CURRENT APPLICATION NUMBER: US/09/993,999
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,316
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-993-999-2

Query Match 43.0%; Score 458; DB 9; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHARGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT----TDWRATLKTIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIAMTKCCNQLDVICYDTCCAN 125
Db 65 YKSDGSKPFRYGYKPSPPNGCGSPLFGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFVSKVEACDSLDVTFVNTVTLGCRPFMNSORAAI 185
Db 121 KNCDEEFQYCLSKICRDVQKTLGTHQVQACETTVELLFDVSVIHLGCKPYLDSORAAI 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 11
US-09-975-374A-2
; Sequence 2, Application US/09975374A
; Patent No. US20020119139A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: CLONING AND RECOMBINANT EXPRESSION OF MAMMALIAN GROUP
; TITLE OF INVENTION: X11 SECRETED PHOSPHOLIPASE A2
; FILE REFERENCE: 1479-R-00
; CURRENT APPLICATION NUMBER: US/09/975,374A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/239,489
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1

Query Match 43.0%; Score 458; DB 9; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHARGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT----TDWRATLKTIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIAMTKCCNQLDVICYDTCCAN 125
Db 65 YKSDGSKPFRYGYKPSPPNGCGSPLFGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFVSKVEACDSLDVTFVNTVTLGCRPFMNSORAAI 185
Db 121 KNCDEEFQYCLSKICRDVQKTLGTHQVQACETTVELLFDVSVIHLGCKPYLDSORAAI 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 12
US-10-147-493-240
; Sequence 240, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHARGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT----TDWRATLKTIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIAMTKCCNQLDVICYDTCCAN 125
Db 65 YKSDGSKPFRYGYKPSPPNGCGSPLFGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
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; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-374A-2

Query Match 43.0%; Score 458; DB 9; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHARGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT----TDWRATLKTIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIAMTKCCNQLDVICYDTCCAN 125
Db 65 YKSDGSKPFRYGYKPSPPNGCGSPLFGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDAKFRWCLXSTCSDLKSLGFVSKVEACDSLDVTFVNTVTLGCRPFMNSORAAI 185
Db 121 KNCDEEFQYCLSKICRDVQKTLGTHQVQACETTVELLFDVSVIHLGCKPYLDSORAAI 180
QY 186 CAEREKEEL 194
Db 181 CHYEKTDL 189

RESULT 12
US-10-147-493-240
; Sequence 240, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSPTSPTDEESYSDW--GLRHARGSFESVNSYFDSFLELLGGKNGVCQ 65
Db 9 LTLULLLMAAVVRCOEQAQT----TDWRATLKTIRNGVHKIDTYLNAALDILGGEDGLCQ 64
QY 66 YRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIAMTKCCNQLDVICYDTCCAN 125
Db 65 YKSDGSKPFRYGYKPSPPNGCGSPLFGV----HLNIGIPSLTKCCNQHDRCYETCGKS 120
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QY 126 KYRCDKAFKRWCLXSTCSDLKRSIGFVSKEVACDSLDVTVENTVWTLGCRPFMNSORAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETVELLFDVSVHLGCKPYLDSQRAACR 180
QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189

RESULT 13
US-10-145-127-240
; Sequence 240, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-145-127-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSGGGLAQSDTSPDTEESYSDW--GLRHLRGSFVSNSYFDSFLELLGKNGVCQ 65
Db 9 LTLTLLMAAVRQEQAOQT---TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMRPGYKPOEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYDTCCAN 125
Db 65 YKCSGSKPFPYRGYKPSPPNGCGSPFLGV---HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDKAFKRWCLXSTCSDLKRSIGFVSKEVACDSLDVTVENTVWTLGCRPFMNSORAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETVELLFDVSVHLGCKPYLDSQRAACR 180
QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189

RESULT 14
US-10-160-503-240
; Sequence 240, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 240
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-160-503-240

Query Match 43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSGGGLAQSDTSPDTEESYSDW--GLRHLRGSFVSNSYFDSFLELLGKNGVCQ 65
Db 9 LTLTLLMAAVRQEQAOQT---TDMRATLKTIRNGVHKIDTYLNAALDLGGEDGLCQ 64
QY 66 YRCRYGKAPMRPGYKPOEPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYDTCCAN 125
Db 65 YKCSGSKPFPYRGYKPSPPNGCGSPFLGV---HLNIGIPSLTKCCNQHDRCYETCGKS 120
QY 126 KYRCDKAFKRWCLXSTCSDLKRSIGFVSKEVACDSLDVTVENTVWTLGCRPFMNSORAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVQACETVELLFDVSVHLGCKPYLDSQRAACR 180
QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189

RESULT 15
US-10-169-395-97
; Sequence 97, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING
; FILE REFERENCE: 01997.015100.US
; CURRENT APPLICATION NUMBER: US/10/169,395
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/JP00/09359
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 150
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; SEQ ID NO 97
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-395-97

Query Match      43.0%; Score 458; DB 12; Length 189;
Best Local Similarity 43.4%; Pred. No. 6.2e-42;
Matches 82; Conservative 42; Mismatches 55; Indels 10; Gaps 3;

QY 8 LVLWLSLGGGLAQSDTSPDTEESYSIW--GLRHLRGSPFVSNSYFDSFLELLGGKNGVCQ 65
Db 9 LLLLLLMAAVKRCQCAQT---TDWRATLKTIRNGVHKIDTYLNAALDGLGGEDGLCQ 64

QY 66 YRCRYGKAPMPRPYKQBPNGCGSYFLGLKVPESMDLGIPIAMTKCNOLDVCYDTCGAN 125
Db 65 YKCSDSGSKPFPYGYKPSPPNGCGSPFLGV-----HLNIGIPSLTKCNQHRCYETCGKS 120

QY 126 KYRCDAKFRWCLXISICSDLKRSIGFVSKVEACDSLYDVTVFNTVTLGCRPFMNSQRAACI 185
Db 121 KNDCEEFQYCLSKICRDVQKTLGLTQHVOACETTVELLFDSVIHLGCKPYLDSQRAACK 180

QY 186 CAEEKEEL 194
Db 181 CHYEKTDL 189
```

Search completed: May 17, 2004, 10:49:38
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:40:14 ; Search time 21 Seconds
(without alignments)
888.626 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLASGFLVLSGGGLAQ.....PFMNSQRAACABEEKEEL 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|---------------------|
| 1 | 87 | 8.2 | 768 | I53821 | P-selectin - rat |
| 2 | 86.5 | 8.1 | 819 | T10355 | hypothetical prote |
| 3 | 84.5 | 7.9 | 389 | I42633 | potential oncogene |
| 4 | 84.5 | 7.9 | 389 | A59392 | Wnt10b protein pre |
| 5 | 84 | 7.9 | 798 | S01659 | integrin beta-1 ch |
| 6 | 84 | 7.9 | 799 | IQMSFB | fibronectin recept |
| 7 | 83.5 | 7.8 | 573 | S36028 | urease (EC 3.5.1.5 |
| 8 | 81 | 7.6 | 2180 | T29764 | insulin-like growt |
| 9 | 80.5 | 7.6 | 304 | A33274 | hypothetical prote |
| 10 | 80.5 | 7.6 | 572 | AC0325 | urease (EC 3.5.1.5 |
| 11 | 80.5 | 7.6 | 1051 | D82428 | chitodextrinase VC |
| 12 | 80 | 7.5 | 414 | B96808 | protein F28K19.2 [|
| 13 | 80 | 7.5 | 799 | JC4126 | integrin beta olig |
| 14 | 80 | 7.5 | 823 | S18968 | cytostatin precurs |
| 15 | 80 | 7.5 | 3051 | S42373 | hypothetical prote |
| 16 | 79.5 | 7.5 | 310 | A60967 | insulin-like growt |
| 17 | 79 | 7.4 | 411 | A65184 | arylsulfatase acti |
| 18 | 79 | 7.4 | 712 | T16338 | hypothetical prote |
| 19 | 78.5 | 7.4 | 293 | T31840 | hypothetical prote |
| 20 | 78.5 | 7.4 | 1820 | A55494 | latent transformin |
| 21 | 78 | 7.3 | 601 | B36346 | fibulin 1 precursor |
| 22 | 78 | 7.3 | 683 | C36346 | fibulin 1 precursor |
| 23 | 78 | 7.3 | 710 | T19054 | zinc finger protei |
| 24 | 77.5 | 7.3 | 153 | T85343 | hypothetical prote |
| 25 | 77.5 | 7.3 | 187 | G85343 | phospholipase A2-1 |
| 26 | 77.5 | 7.3 | 1054 | T10933 | chitinase (EC 3.2. |
| 27 | 77 | 7.2 | 353 | I51572 | maternal protein - |
| 28 | 77 | 7.2 | 411 | B91220 | probable arylsulfa |
| 29 | 77 | 7.2 | 411 | D86066 | probable arylsulfa |

ALIGNMENTS

RESULT 1

I53821

P-selectin - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Aug-2002

C:Accession: I53821

R:Auchampach, J.A.; Oliver, M.G.; Anderson, D.C.; Manning, A.M.

Gene 145, 251-255, 1994

A:Title: Cloning, sequence comparison and in vivo expression of the gene encoding rat P

A:Reference number: I53821; MUID:94333817; PMID:7520013

A:Accession: I53821

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-768 <RES>

A:Cross-references: GB:I23088; NID:g349552; PID:AAA60325.1; PID:g349553

C:Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology;

F:32-158/Domain: C-type lectin homology <LCH>

F:163-194/Domain: EGF homology <EGF>

F:262-319/Domain: complement factor H repeat homology <FHR>

F:510-567/Domain: complement factor H repeat homology <FH06>

F:580-637/Domain: complement factor H repeat homology <FH07>

F:642-699/Domain: complement factor H repeat homology <FH08>

| | | | | |
|-----------------------|-------|--|-------|-----------------------------------|
| Query Match | 8.2% | Score 87; | DB 2; | Length 768; |
| Best Local Similarity | 26.4% | Pred. No. 3.3; | | |
| Matches | 37; | Conservative | 9; | Mismatches 42; Indels 52; Gaps 8; |
| Qy | 38 | HLRGSFE-----SVNSYFDFLELLGGKNGVCOYRCRYGKAMPFRPGYKQEPNGCGS | 90 | |
| Db | 525 | HVHGFEFVGSTCFSCNEEF---ELLGSRNVECTVSGRWSPPTCKG----- | 569 | |
| Qy | 91 | YFLGLKVPESMDLIPAMT-----KCCNOLD-----VCYDTC-----GANKYRCD | 130 | |
| Db | 570 | -VTLPLVP---SVRCPALTPFGQMTSCRHLESGFNNTTCYFGCKTFTLRGANSURFCG | 625 | |
| Qy | 131 | AKFRW-----CLXSIGSDL | 144 | |
| Db | 626 | ASGQWTATPVCRAVKSEL | 645 | |

RESULT 2

T10355

hypothetical protein 86 - Orgyia pseudotsugata nuclear polyhedrosis virus

C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C:Accession: T10355

R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.

Virolgy 229, 381-399, 1997

A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis

A:Reference number: Z17011; MUID:97271300; PMID:9126251

A:Accession: T10355

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-819 <AHR>

A:Cross-references: EMBL:U75930; NID:g2934903; PID:g1911332

Query Match 8.1%; Score 86.5; DB 2; Length 819;

Best Local Similarity 24.7%; Pred. No. 3.9;

Matches 45; Conservative 22; Mismatches 62; Indels 53; Gaps 9;

Qy 46 VNSYF-----DSFLELGGKNGV--QYRCRYGKAPMPREGYKQBPNGCGSYFLGLKV 97

Db 234 VLAYFPETLRVNEFVECKGKHVVARCPDQOVFORALMTVCQTHPCAFNGAGHTYI----- 289

Qy 98 PESMDLGPAMTKCNQLDVCYDTC-----CAN-KYRCDAKFRCLXISICSLKXSLG-- 149

Db 290 --TADIGDAQFCKLNDREAQLITCINRVGADGQYACSGDAR-----CADLPDGTGRL 341

Qy 150 -----FVSKVEACDS-----LVDFVNTVMTLGRPFMNSQRAACI 185

Db 342 MHTHTDDTFEYVSGTICDNYNVISEIECDTGNVLNKLKFNKFTLGAQ--FPREVLDAGV 400

Qy 186 CA 187

Db 401 CA 402

RESULT 3

149263

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999

C:Accession: I49263

R:Lee, F.S.; Lane, T.F.; Kuo, A.; Shackelford, G.M.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 92, 2268-2272, 1995

A:Title: Insertional mutagenesis identifies a member of the Wnt gene family as a candidate

A:Reference number: I49263; MUID:95199333; PMID:7892260

A:Accession: I49263

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-389 <RES>

A:Cross-references: EMBL:U20658; NID:g1020149; PIDN:AAA80110.1; PID:g677918

C:Genetics:

A:Superfamily: int-1 transforming protein

Query Match 7.9%; Score 84.5; DB 2; Length 389;

Best Local Similarity 22.0%; Pred. No. 3.1;

Matches 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5;

Qy 59 GKXGVCQYRCRYGKAPMPR-----LGIPAMT-KCCNQLDVCYDTCGA-----PGYKQBPNGCGSY 91

Db 251 GTSGCQFKTCWRAAPEFRAIGALRERLSRAIFIDITHNRNSGAFQPLRPRLSGELVY 310

Qy 92 FLGLKVPESMD-----LGIPAMT-KCCNQLDVCYDTCGA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTLGSPTGRACNKTSLRLDGGSLCCGGRGHNVLRQTRVERCHCRF 368

Qy 134 RWCLXISICDLK 145

Db 369 HWCCYVLCDECK 380

RESULT 4

A59392

Wnt10b protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C:Accession: A59393; A59392

R:Lee, F.S.; Lane, T.F.; Kuo, A.; Shackelford, G.M.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 92, 2268-2272, 1995

A:Title: Insertional mutagenesis identifies a member of the Wnt gene family as a candidate

A:Reference number: A59393; MUID:95199333; PMID:7892260

A:Accession: A59393

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-389 <LEE>

A:Cross-references: GB:U20658; NID:g1020149; PID:g1351425; PIDN:AAA80110.1

R:Wang, J.; Shackelford, G.M.

Oncogene 13, 1537-1544, 1996

A:Title: Murine Wnt10a and Wnt10b: cloning and expression in developing limbs, face and

A:Reference number: A59392; MUID:96269404; PMID:8875992

A:Accession: A59392

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-389 <WAN>

A:Cross-references: GB:U61970; NID:g1546014; PID:g1546015; PIDN:AA808086.1

A:Note: proto-oncogene, potential transforming capacity, secreted protein, developmental

C:Superfamily: int-1 transforming protein

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-389/Product: Wnt10b protein #status predicted <MAR>

Query Match 7.9%; Score 84.5; DB 2; Length 389;

Best Local Similarity 22.0%; Pred. No. 3.1;

Matches 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5;

Qy 59 GKXGVCQYRCRYGKAPMPR-----LGIPAMT-KCCNQLDVCYDTCGA-----PGYKQBPNGCGSY 91

Db 251 GTSGCQFKTCWRAAPEFRAIGALRERLSRAIFIDITHNRNSGAFQPLRPRLSGELVY 310

Qy 92 FLGLKVPESMD-----LGIPAMT-KCCNQLDVCYDTCGA-----NKYRCDAKF 133

Db 311 F--EKSPDFCERDPTLGSPTGRACNKTSLRLDGGSLCCGGRGHNVLRQTRVERCHCRF 368

Qy 134 RWCLXISICDLK 145

Db 369 HWCCYVLCDECK 380

RESULT 5

S01659

Integrin beta-1 chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Aug-1999

C:Accession: S01659

R:Tominaga, S.I.

FEBS Lett. 238, 315-319, 1988

A:Title: Murine mRNA for the beta-subunit of integrin is increased in BALB/c-3T3 cells

A:Reference number: S01659; MUID:89005707; PMID:3262537

A:Accession: S01659

A:Molecule type: mRNA

A:Residues: 1-798 <TOM>

A:Cross-references: EMBL:Y00769; NID:g52721; PIDN:CAA68738.1; PID:g52722

A:Note: the authors translated the codon ATT for residue 696 as Leu

C:Superfamily: integrin beta chain; laminin-type EGF-like homology

C:Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-798/Product: Integrin beta-1 chain #status predicted <MAT>

Query Match 7.9%; Score 84; DB 2; Length 798;

Best Local Similarity 26.8%; Pred. No. 6.5;

Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;

Qy 26 DTEESYSDWGLRHRLGSP-ESVNSYFDSFLELLGGKNGVCQYRCRYGKAPMPREGYKQPE 84

Db 543 NTNEIYS-----GKFCEDNFCDNRSLICGGNGVC--RCRVCE----- 580

Qy 85 PNGCGSYFLGLKVPESMDLG--IPAMTKCCNQLDVCYDTCGANKYRC-DAKFRWCLXSLC 141

Db 581 ---CYPNTGTGACDCSLDTGFCILASNGQICNGRGIC--ECGACK--CTDPFKQ---GFTC 630

Qy 142 SDLKESLGFVSKVEACDSLVDTVFNTVWTLGCRPFMNSQRAACICAE 189

Db 631 ETCQCTCLGVCAEHKEC-----VQCRAF-NKGEKKDTCQAE 664

RESULT 6

IJMSFB

fibronectin receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C:Accession: P10104; B60597
R:Holters, V.M.; Ruff, T.G.; Parks, D.L.; McDonald, J.A.; Ballard, L.L.; Brown, E.J.
J. Exp. Med. 169, 1589-1605, 1989
A:Title: Molecular cloning of a murine fibronectin receptor and its expression during in
for histocompatibility complex class II.
A:Reference number: P10103; MUID:89235580; PMID:2523953
A:Accession: P10104
A:Molecule type: mRNA
A:Residues: 1-799 <HOL>
A:Cross-references: GB:X15202; GB:Y00818; NID:G50986; PIDN:CAA33272.1; PID:G762977
A:Experimental source: strain BALB/c
A:Note: the cDNA clone was missing the first nucleotide of Met-1
R:Ryseck, R.P.; Macdonald-Bravo, H.; Zerlial, M.; Bravo, R.
Exp. Cell Res. 180, 537-545, 1989
A:Title: Coordinate induction of fibronectin, fibronectin receptor, tropomyosin, and act
A:Reference number: A60597; MUID:89121031; PMID:2521606
A:Accession: B60597
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 596-799 <RYS>
A:Comment: The receptor is a heterodimer of alpha and beta chains.
C:Superfamily: integrin beta chain; laminin-type EGF-like homology
C:Keywords: Cell adhesion; duplication; glycoprotein; heterodimer; receptor; transmembra
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-799/Product: fibronectin receptor beta chain #status predicted <MAT>
F:21-729/Domain: extracellular #status predicted <EXT>
F:730-752/Domain: transmembrane #status predicted <TRA>
F:753-799/Domain: intracellular #status predicted <INT>
F:50,94,97,212,269,363,406,417,482,521,585,670/Binding site: carbohydrate (Asn) (covalen
Query Match 7.9%; Score 84; DB 1; Length 799;
Best Local Similarity 26.8%; Pred. No. 6.5;
Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;
QY 26 DTEESYSDWGLRHLSGSP--ESVNSYFDSLELLGGKNGVCQYRCYRGKAPMPRGYKPOE 84
DB 544 NTNEIYS-----GKFCEDNFNCDNRSLGICGGNGVC--RCRVCE----- 581
QY 85 PNGCGSYFLGLKVPESMDLIG--IPAMTKCNQDVCYDTGANKYRC-DAKFRWCLXSTC 141
DB 582 ---CYFNTYGSACDGLDTPCLASNGQICNGRGIC--ECGACK--CTDPKFKQ---GPTC 631
QY 142 SDLKRSGLGVSKVEACDLSLVDVTFVNTVTLGCRPFMNSQRAACICAE 189
DB 632 ETCQCLGVCAEHKEC-----VQCRAP-NKGEKDTCAQE 665
RESULT 7
S36028
Urease (EC 3.5.1.5) yeuC - Yersinia enterocolitica
N:Alternate names: yeuC protein
C:Species: Yersinia enterocolitica
C>Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 06-Jan-2003
C:Accession: S36028; S31419
R:Skurnik, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S36028
A:Accession: S36028
A:Molecule type: DNA
A:Residues: 1-573 <SKU>
A:Cross-references: EMBL:Z18865; NID:G1016360; PIDN:CAA79316.1; PID:G296319
R:Skurnik, M.; Bateford, S.; Mertz, A.; Schilz, E.; Toivanen, P.
submitted to the EMBL Data Library, December 1992
A:Description: The putative arithrogenic cationic 19 kD antigen of Yersinia enterocolib
A:Reference number: S31417
A:Accession: S31419
A:Molecule type: DNA
A:Residues: 1-59 <SK2>
A:Cross-references: EMBL:Z18865
C:Genetics:

A:Gene: yeuC
C:Superfamily: urease, alpha subunit; urease 62K chain homology
C:Keywords: hydrolase
F:4-556/Domain: urease 62K chain homology <U62>
Query Match 7.8%; Score 83.5; DB 2; Length 573;
Best Local Similarity 25.8%; Pred. No. 5.4;
Matches 31; Conservative 17; Mismatches 49; Indels 23; Gaps 5;
QY 15 GGGLAQSDTSPDTESYSDWGLRHLSGSPES--VNSYFDSLELLGGKNGVCQYRCYRGK 72
DB 162 GGGTGPTDGTGTTTPGPNIRQLRSVEGLPVN-----VGILGKNS-----YGR 208
QY 73 APMPRP-----GYKQPPNGCGSYFL--GLKVPESMDLIGIPAMTKCNQDVCYDTGCA 124
DB 209 GPLLEQATAGVGVKVEDWGTATANALRHSLRMADEMDLIQSVHTDSLNECGYVEETIDA 268
RESULT 8
T29764
Hypothetical protein T21E3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T29764
R:Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid T21E3.
A:Reference number: Z20681
A:Accession: T29764
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2180 <DUZ>
A:Cross-references: EMBL:AF003133; PIDN:AA854138.1; GSPDB:GN00019; CESP:T21E3.3
A:Experimental source: strain Bristol N2; clone T21E3
C:Genetics:
A:Gene: CESP:T21E3.3
A:Map position: 1
A:Introns: 400/2; 1608/3; 1644/1; 1674/3; 1686/2; 1731/2; 2073/1; 2098/2; 2146/3
C:Superfamily: LDL receptor ligand-binding repeat homology
F:15-49/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:51-85/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:90-132/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:149-185/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:190-225/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:229-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:285-316/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:323-359/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:369-405/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:816-856/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:861-903/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:908-943/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F:948-987/Domain: LDL receptor ligand-binding repeat homology <LDL13>
F:993-1027/Domain: LDL receptor ligand-binding repeat homology <LDL14>
F:1031-1063/Domain: LDL receptor ligand-binding repeat homology <LDL15>
F:1126-1165/Domain: LDL receptor ligand-binding repeat homology <LDL16>
F:1172-1209/Domain: LDL receptor ligand-binding repeat homology <LDL17>
F:1213-1246/Domain: LDL receptor ligand-binding repeat homology <LDL18>
Query Match 7.6%; Score 81; DB 2; Length 2180;
Best Local Similarity 24.8%; Pred. No. 31;
Matches 29; Conservative 16; Mismatches 30; Indels 42; Gaps 8;
QY 69 RYKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLIGIPAMTKCNQDVCYD-----T 121
DB 8 KYCSTRVCRPGY-----FNCNGN---GLCIPEQ-----KVCNRINDCANFADESNC 50
QY 122 CGANKYRCDAKFRWCLXSTCSDLKRSGLGVSKVEACDLSLVDVTFVNTVTLGCRPFM 178
DB 51 CNNEFRQCS-----GACIPSKAR---CNHMQDCNDASDEI-----GC-PFRN 89
RESULT 9
A33274

insulin-like growth factor-binding protein 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 07-Jul-2003
 C:Accession: A33274; A40149; A25016; C33570; A31355; A61119; C40403; A49170
 R:Brown, A.L.; Chiarotti, L.; Orłowski, C.C.; Mehman, T.; Burgess, W.H.; Ackerman, E.J.
 J. Biol. Chem. 264, 5148-5154, 1989
 A>Title: Nucleotide sequence and expression of a cDNA clone encoding a fetal rat binding
 A:Reference number: A33274; MUID:89174801; PMID:2538475
 A:Accession: A33274
 A:Molecule type: mRNA
 A:Residues: 1-304 <BRO>
 A:CROSS-references: GB:J04486; NID:G203175; PIDN:AAA40829.1; PID:G203176
 R:Margot, J.B.; Binkert, C.; Mary, J.L.; Landwehr, J.; Heinrich, G.; Schwander, J.
 Mol. Endocrinol. 3, 1053-1060, 1989
 A>Title: A low molecular weight insulin-like growth factor binding protein from rat: cDN
 A:Reference number: A40149; MUID:90014825; PMID:2477691
 A:Accession: A40149
 A:Molecule type: protein
 A:Residues: 1-297 'A', 299-304 <MAR>
 A:CROSS-references: GB:M31672; NID:G204734; PIDN:AAA41381.1; PID:G204735
 R:McTotta, C.; Macdonald, R.G.; Brackett, J.L.; Mole, J.E.; Anderson, J.K.; Czech, M.P.
 J. Biol. Chem. 261, 11180-11188, 1986
 A>Title: Purification and amino-terminal sequence of an insulin-like growth factor-bindin
 A:Reference number: A25016; MUID:86278218; PMID:2426267
 A:Accession: A25016
 A:Molecule type: protein
 A:Residues: 38-68 <MOT>
 R:Shimonaka, M.; Schroeder, R.; Shimazaki, S.; Ling, N.
 Biochem. Biophys. Res. Commun. 165, 189-195, 1989
 A>Title: Identification of a novel binding protein for insulin-like growth factors in ad
 A:Reference number: A33570; MUID:90073708; PMID:2480123
 A:Accession: C33570
 A:Molecule type: protein
 A:Residues: 35-39, 'X', 41-42, 'X', 44-50, 'X', 52-58, 'X', 60-64 <SHI>
 R:Wang, J.F.; Hampton, B.; Mehman, T.; Burgess, W.H.; Rechler, M.M.
 Biochem. Biophys. Res. Commun. 157, 718-726, 1988
 A>Title: Isolation of a biologically active fragment from the carboxy terminus of the fe
 A:Reference number: A31355; MUID:89076308; PMID:2974285
 A:Accession: A31355
 A:Molecule type: protein
 A:Residues: 178-204 <WAN>
 R:Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, M.K.
 Endocrinology 129, 1066-1074, 1991
 A>Title: Developmental expression of rat insulin-like growth factor binding protein-2 by
 A:Reference number: A61119; MUID:91309520; PMID:1713158
 A:Accession: A61119
 A:Molecule type: protein
 A:Residues: 35-67 <OLS>
 R:Shimasaki, S.; Shimonaka, M.; Zhang, H.P.; Ling, N.
 J. Biol. Chem. 266, 10646-10653, 1991
 A>Title: Identification of five different insulin-like growth factor binding proteins (I
 A:Reference number: A40403; MUID:91244847; PMID:1709938
 A:Accession: C40403
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 35-39, 'X', 41-42, 'X', 44-50, 'X', 52-57 <SH2>
 R:Park, J.H.Y.; McCusker, R.H.; Vanderhoof, J.A.; Mohammadpour, H.; Harty, R.F.; MacDona
 Endocrinology 131, 1359-1368, 1992
 A>Title: Secretion of insulin-like growth factor II (IGF-II) and IGF-binding protein-2 b
 A:Reference number: A49170; MUID:92371335; PMID:1380441
 A:Accession: A49170
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 35-39, 'X', 41-42, 'X', 44-50, 'X', 52 <PAR>
 C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h
 C:Keywords: plasma
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-304/Product: insulin-like growth factor binding protein 2 #status experimental <MAT
 F:206-285/Domain: thyroglobulin type I repeat homology <THY1>
 Query Match 7.6%; Score 80.5; DB 2; Length 304;
 Best Local Similarity 22.5%; Pred. No. 5.7;
 Matches 39; Conservative 25; Mismatches 60; Indels 49; Gaps 9;

Qy 26 DTBESYSDWGLRHRLGSGFESVNSYFDSFLELLGGKNGVQYRCYKAPMPGKYK---- 81
 Db 129 DSEDDHSEGL-----VENHVDGTMMMLGGSSA-----GRKP-PKSGMKELAV 170
 Qy 82 -----POEPNGCGSYFLGLKVPESMDLGPAMTKCCNOLDVCYDPCGANKYRCDAKFR 134
 Db 171 FREKVNQHRQMGKGAHLSLEBPKL-RPPPARTPCQELDQVLERISTWRLPDD---R 226
 Qy 135 WCLXSICDLKSLRSLGFSVKEACDLSLVDVTNVTWL-GCRPFMNSORACIC 186
 Db 227 GPLFHLYS-----LHPCNDK-----HGLYNLKQCKMSLNGRGECWC 264
 RESULT 10
 AC0325
 urease (EC 3.5.1.5) alpha chain [imported] [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 06-Jan-2003
 C:Accession: AC0325
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AC0325
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-572 <KUR>
 A:CROSS-references: GB:AL590842; PIDN:CAC92906.1; PID:G15980647; GSPDB:GN00175
 C:Genetics:
 A:Gene: ureC
 C:Superfamily: urease, alpha subunit; urease 62K chain homology
 C:Keywords: hydrolase
 Query Match 7.6%; Score 80.5; DB 2; Length 572;
 Best Local Similarity 25.0%; Pred. No. 10;
 Matches 30; Conservative 18; Mismatches 49; Indels 23; Gaps 5;
 Qy 15 GGGAAQSDTSPDTBESYSDWGLRHRLGSGFESVNSYFDSFLELLGGKNGVQYRCYK 72
 Db 161 GGGIGPTDGTGTGTTVTPGPMNIQMLRSIEGLPVN-----VGILKGNS-----YGR 207
 Qy 73 APMPRP-----GYKQPQPCGSGYFL--GLKVPESMDLGPAMTKCCNOLDVCYDTCGA 124
 Db 208 GPLLEQAIAGVVGKVEDWGTATNALEHRLMADEVDIQSVHTDSLNECGYVEDTIDA 267
 RESULT 11
 chitodextrinase VCA0700 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 D82428
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: D82428
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: D82428
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1051 <HEI>
 A:CROSS-references: GB:AE003853; NID:G9658111; PIDN:AAF96599.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VCA0700
 A:Map position: 2
 Query Match 7.6%; Score 80.5; DB 2; Length 1051;
 Best Local Similarity 24.8%; Pred. No. 18;

Matches 27; Conservative 14; Mismatches 35; Indels 33; Gaps 4;
QY 14 LGGLAQSDTSPPTESY-----SDWGLRLHSGSPES-----VNSYFD 51
Db 569 VGHNAALYDTGKDSLAOMNVYTAQYGGIGYLTNDWXYHFRGSPAGRINTGVPIYTR 628
QY 52 SFLELGGKNGVCQYRCRYKAMPKPR-----PGYKQPEPNCGSYFLGL 95
Db 629 GWOGVTGGNGL-----WGRAALPNQNLCAPTGEGEKNGCHGATGI 671
RESULT 12
B96808
protein F28K19.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B96808
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Lueros, J.S.; Matti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96808
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <STO>
A:Cross-references: GB:AE005173; NID:g6573782; PIDN:AAF17702.1; GSPDB:GN00141
C:Genetics:
A:Gene: F28K19.2
A:Map position: 1
Query Match 7.5%; Score 80; DB 2; Length 414;
Best Local Similarity 29.1%; Pred. No. 8.5;
Matches 32; Conservative 9; Mismatches 49; Indels 20; Gaps 6;
QY 89 GSVFLGLKVPESMDLGLTPAMTKCNQLDVCYDTGANKYRCDAKFRCLXISCSDLKRL 148
Db 298 GSWFGLGLEHIDRNF-----CGTPDCRWKAAGDV-CVASFWSGSGICKSVSR-- 349
QY 149 GFVSKV--EACDSLVDTVNTVTLGCRPFMNSQRAACI-----CAEEK 191
Db 350 ---WKIVHEVCSEGEAVWNLT--LQVPIILNITLIDCYKKGKEREER 394
RESULT 13
JC4126
integrin beta oligodendroglia chain precursor - rat
N:Alternate names: integrin b1 chain precursor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Aug-1999
C:Accession: JC4126
R:Malek-Hedayat, S.; Rome, L.H.
Gene 158, 287-290, 1995
A:Title: Cloning and sequence of the cDNA encoding the rat oligodendrocyte integrin beta
A:Reference number: JC4126; MUID:95331632; PMID:7541764
A:Accession: JC4126
A:Molecule type: mRNA
A:Residues: 1-799 <MAL>
A:Cross-references: GB:U12309; NID:g520565; PIDN:ABA86669.1; PID:g520566
C:Comment: This protein belongs to a superfamily of heterodimeric cell-surface glycoprob
C:Superfamily: integrin beta chain; laminin-type EGF-like homology
C:Keywords: glycoprotein; oligodendrocyte; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-799/Product: integrin beta oligodendroglia chain #status predicted <MAT>
F:730-752/Domain: transmembrane #status predicted <TM>
F:570,94,97,212,269,363,406,417,482,521,585,670/Binding site: carbohydrate (Asn) (covalen

Query Match 7.5%; Score 80; DB 2; Length 799;
Best Local Similarity 26.6%; Pred. No. 15;
Matches 45; Conservative 16; Mismatches 56; Indels 52; Gaps 12;
QY 26 DTEESYSDWGLRLHRSF-ESVNSYFDSFLELGGKNGVCQYRCRYKAMPKPRPGYKQ 84
Db 544 NTEIYS-----GKFCECFNDRSNGLTCGGNGVC--RCRVCE----- 581
QY 85 PNGCGSYFLGLKVPESMDLGLIPAMT---KCCNQLDVCYDTGANKYRC-DAKFRWCLXSI 140
Db 582 ---CYPNTYTGACDCSLDT-VPCVAINGQICNGRGIC--ECGACK--CTDPKQ---GPT 630
QY 141 CSDLKRSGLGFVSKVEACDSLVDTVNTVTLGCRPFMNSQRAACICAE 189
Db 631 CFTCQTCLGVCAEHKEC-----VQCRAF-NKGEKKDTCQAE 665
RESULT 14
S18968
cyttestin precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: I48784; S18968
R:Senftleben, A.; Wallat, S.; Lemaire, L.; Heinlein, U.A.O.
Dev. Growth Differ. 36, 49-58, 1994
A:Title: Pre and postmeiotic germ cell specific expression of TAZ83, a gene encoding a f
A:Reference number: I48784
A:Accession: I48784
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-823 <RES>
A:Cross-references: EMBL:X64227; NID:g54264; PID:g54265
C:Genetics:
A:Gene: TAZ83
C:Superfamily: mouse meltrin alpha; disintegrin homology
F:395-480/Domain: disintegrin homology <DIS>
Query Match 7.5%; Score 80; DB 2; Length 823;
Best Local Similarity 26.3%; Pred. No. 16;
Matches 35; Conservative 16; Mismatches 44; Indels 38; Gaps 10;
QY 81 KPDPNGCGSYFLGLKVPESMDLGLIP---AMTKCNQLD---VCYDTGANKYRCDAKFR 134
Db 392 QPQGGSYCGNHL--LEVPEQDCGPPETCTHKCCNPKDCTLDAAQCGTGPC-CDK-R 446
QY 135 WCLXS---ICSDLKRSGLGFVSKVEACDSLVDTVNTVTLGCRPF-----MNSQRA 182
Db 447 TCTIAERGLCRKSKQDCF---PEFCNG-----ETEGCAPDTKAADLEPCNNETA 494
QY 183 AC---ICAEERE 192
Db 495 YCFGVCRDPDRQ 507
RESULT 15
S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S42373
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42373
A:Molecule type: DNA
A:Residues: 1-3051 <SMI>
A:Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C:Genetics:
A:Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
C:Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin t
F:512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F:754-793/Domain: fibronectin type II repeat homology <2FI>
F:1201-1244/Domain: EGF homology <EGF>

Query Match 7.5%; Score 80; DB 2; Length 3051;
Best Local Similarity 24.0%; Pred. No. 52; Mismatches 57; Indels 64; Gaps 9;
Matches 43; Conservative 15; Mismatches 57; Indels 64; Gaps 9;
QY 42 SPESVNSYFDSFELELGGKNGVCQYRCRYGKAPMPRPGYKQOEP-----NGCGS 90
Db 1960 SLNSCSAFADCFDE---ENG---YRCRC-----RNGYHDDDDPAHPGHRCSFMINCEDS 2006
QY 91 YFGLKVPESMDLGIPTAMTKCCNQLDVCYDTGANKYRCDAKF-----RWCLXSI 140
Db 2007 SNL-----NDCDRNANCIDTAGGYDCACKAPYRDEGPPQSPGRCRLNE 2050
QY 141 CSDLKRSGLGVSKVEACDSLVD-TVFNVTWTLGCR-----PFMNSORAAACIAEEBKEE 193
Db 2051 CLNPNRN-----TCDRNACRDLIDGYTCTCRHGFDQSPNPQEPGRICIEFQOEE 2101

Search completed: May 17, 2004, 10:44:17
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 10:36:28 ; Search time 17 seconds
(without alignments)
594.212 Million cell updates/sec

Title: US-10-621-401-145

Perfect score: 1066

Sequence: 1 MKLAGFLVWLGGGLAQ.....PFMNSQRAACICAEKEEKL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|------------|---------------------|
| 1 | 1053.5 | 98.8 | 195 | PA2Z HUMAN | Q9bx93 homo sapien |
| 2 | 946.5 | 88.8 | 195 | PA2Z MOUSE | Q99p27 mus musculus |
| 3 | 467 | 43.8 | 192 | PA2Y MOUSE | Q9ep22 mus musculus |
| 4 | 458 | 43.0 | 189 | PA2Y HUMAN | Q9bzm1 homo sapien |
| 5 | 88 | 8.3 | 396 | POOE RAHAQ | O33506 rahnella aq |
| 6 | 87 | 8.2 | 768 | LEM3 RAT | P98106 rattus norv |
| 7 | 86.5 | 8.1 | 443 | FBL4 CRIGR | O55058 cricetus |
| 8 | 86.5 | 8.1 | 819 | Y083 NPVOP | O10336 orgyia pseu |
| 9 | 84.5 | 7.9 | 389 | WN1B MOUSE | P48614 mus musculus |
| 10 | 84 | 7.9 | 798 | ITB1 MOUSE | P09055 mus musculus |
| 11 | 83.5 | 7.8 | 443 | FBL4 HUMAN | O95967 homo sapien |
| 12 | 83.5 | 7.8 | 571 | URE1 YEREN | P31494 yersinia en |
| 13 | 82.5 | 7.7 | 389 | WN1B HUMAN | O00744 homo sapien |
| 14 | 81.5 | 7.6 | 571 | URE1 YERPS | P52313 yersinia ps |
| 15 | 80.5 | 7.6 | 304 | IBP2 RAT | P12843 rattus norv |
| 16 | 80.5 | 7.6 | 431 | NOCT HUMAN | Q9uk39 homo sapien |
| 17 | 80.5 | 7.6 | 443 | FBL4 MOUSE | O9wtj9 mus musculus |
| 18 | 80.5 | 7.6 | 571 | URE1 YERPE | O9zfz9 yersinia pe |
| 19 | 80 | 7.5 | 799 | ITB1 RAT | P49134 rattus norv |
| 20 | 80 | 7.5 | 3787 | MUAS CAEEL | P34576 caenorhabdi |
| 21 | 79.5 | 7.5 | 429 | NOCT MOUSE | O35710 mus musculus |
| 22 | 79 | 7.4 | 411 | ASLB ECOLI | P25550 escherichia |
| 23 | 78 | 7.3 | 703 | FBL1 HUMAN | P23142 homo sapien |
| 24 | 77.5 | 7.3 | 2471 | NTC2 HUMAN | O04721 homo sapien |
| 25 | 77 | 7.2 | 353 | WN11 XENLA | P49893 xenopus lae |
| 26 | 77 | 7.2 | 768 | LEM3 MOUSE | Q01102 mus musculus |
| 27 | 77 | 7.2 | 773 | ITB1 BOVIN | P53712 bos taurus |
| 28 | 77 | 7.2 | 798 | ITB1 FELCA | P53713 felis silve |
| 29 | 76.5 | 7.2 | 2470 | NTC2 MOUSE | O35516 mus musculus |
| 30 | 76 | 7.1 | 1195 | KDGD HUMAN | O16760 homo sapien |
| 31 | 75.5 | 7.1 | 142 | PA2Z HELSU | P80003 heloderma s |
| 32 | 75.5 | 7.1 | 835 | CD97 HUMAN | P48960 homo sapien |
| 33 | 75.5 | 7.1 | 1025 | CA16 MOUSE | Q04857 mus musculus |

| | | | | | | |
|----|------|-----|-----|---|------------|---------------------|
| 34 | 75 | 7.0 | 130 | 1 | TAT SIWML | P05911 simian immu |
| 35 | 75 | 7.0 | 144 | 1 | PA2A HUMAN | P14555 homo sapien |
| 36 | 74.5 | 7.0 | 145 | 1 | PA2M CAVPO | P47711 cavia porce |
| 37 | 74.5 | 7.0 | 317 | 1 | IBF2 SHEEP | Q29400 ovis aries |
| 38 | 74.5 | 7.0 | 371 | 1 | WNT1 XENLA | P10108 xenopus lae |
| 39 | 74.5 | 7.0 | 509 | 1 | PA23 HUMAN | Q9nz20 homo sapien |
| 40 | 74.5 | 7.0 | 577 | 1 | TRBM MOUSE | P15306 mus musculus |
| 41 | 73.5 | 6.9 | 253 | 1 | NOCT RAT | Q9et55 rattus norv |
| 42 | 73.5 | 6.9 | 305 | 1 | IBP2 MOUSE | P47877 mus musculus |
| 43 | 73.5 | 6.9 | 328 | 1 | IBF2 HUMAN | P18065 homo sapien |
| 44 | 73.5 | 6.9 | 417 | 1 | WN1A HUMAN | Q9gzts homo sapien |
| 45 | 73.5 | 6.9 | 777 | 1 | UNC8 CAEEL | Q21974 caenorhabdi |

ALIGNMENTS

| | | | | | | | | | |
|--|--|-----------|---|-------------------------------|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| ID | PA2Z HUMAN | STANDARD; | PRT; | 195 AA. | | | | | |
| AC | Q9BX53; Q96Q99; | | | | | | | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | | | | | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | | | | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | | | | | | |
| DE | Group XIII secretory phospholipase A2-like protein precursor (GXIII sPLA2-like). | | | | | | | | |
| GN | PLA2G13 OR FKSG71. | | | | | | | | |
| OS | Homo sapiens (Human). | | | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | | | | | |
| OX | NCBI_TaxID=9606; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RA | Takahashi K.; | | | | | | | | |
| RT | "Cloning of human group XIII secreted phospholipase A2."; | | | | | | | | |
| RL | Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases. | | | | | | | | |
| RN | [2] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RA | Wang Y.-G., Gong L.; | | | | | | | | |
| RT | "Cloning and characterization of FKSG71, a novel gene encoding group XIII secreted phospholipase A2."; | | | | | | | | |
| CC | Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases. | | | | | | | | |
| CC | -!- FUNCTION: Not known; does not seem to have catalytic activity. | | | | | | | | |
| CC | -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity). | | | | | | | | |
| CC | -!- SUBCELLULAR LOCATION: Secreted. | | | | | | | | |
| CC | -!- SIMILARITY: Belongs to the phospholipase A2 family. | | | | | | | | |
| ----- | | | | | | | | | |
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| ----- | | | | | | | | | |
| EMBL; AF349540; AAK30168.1; - | | | | | | | | | |
| EMBL; AF339053; AAL09472.1; - | | | | | | | | | |
| Genew; HGNC:18555; PLA2G13 | | | | | | | | | |
| InterPro; IPR000886; ER_target_S | | | | | | | | | |
| InterPro; IPR001211; PhospholipaseA2 | | | | | | | | | |
| PROSITE; PS00119; PA2 ASP; FALSE NEG. | | | | | | | | | |
| PROSITE; PS00118; PA2_HIS; FALSE NEG. | | | | | | | | | |
| PROSITE; PS00014; ER_TARGET; UNKNOWN_1 | | | | | | | | | |
| Calcium; Signal. | | | | | | | | | |
| SIGNAL | 1 | 19 | POTENTIAL. | | | | | | |
| CHAIN | 20 | 195 | GROUP XIII SECRETORY PHOSPHOLIPASE A2 - | | | | | | |
| FT | LIKE PROTEIN. | | | | | | | | |
| FT | METAL | 89 | 89 | CALCIUM (VIA CARBONYL OXYGEN) | | | | | |
| FT | (BY SIMILARITY). | | | | | | | | |
| FT | METAL | 91 | 91 | CALCIUM (VIA CARBONYL OXYGEN) | | | | | |
| FT | (BY SIMILARITY). | | | | | | | | |
| FT | METAL | 93 | 93 | CALCIUM (VIA CARBONYL OXYGEN) | | | | | |
| FT | (BY SIMILARITY). | | | | | | | | |

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FT METAL 116 116 CALCIUM (BY SIMILARITY).
FT CONFLICT 157 MISSING (IN REF. 1).
SQ SEQUENCE 195 AA; 21659 MW; C00C817F81D68A70 CRC64;

Query Match 98.8%; Score 1053.5; DB 1; Length 195;
Best Local Similarity 99.0%; Pred. No. 8.9e-96;
Matches 193; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MKLASGFLVWLSLGGGLAQSDTSPTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60
DB 1 MKLASGFLVWLSLGGGLAQSDTSPTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIKPKATKCCNQLDVYD 120
DB 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIKPKATKCCNQLDVYD 120
QY 121 TCGANKYRCDAKFRWCLXSLKSLGSLGFVSKVE-ACDSLVDTVFTNTVTLGCRPFMNS 179
DB 121 TCGANKYRCDAKFRWCLXSLKSLGSLGFVSKVE-ACDSLVDTVFTNTVTLGCRPFMNS 180
QY 180 QRAACICABEEKEEL 194
DB 181 QRAACICABEEKEEL 195

RESULT 2
PA2Z_MOUSE STANDARD; PRT; 195 AA.
AC Q99P27;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Group XIII secretory phospholipase A2-like protein precursor (GXIII
DE sPLA2-like)
GN PLA2g13 OR FKSG71.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 x DBA;
RA Wang Y.-G., Gong L.;
RT "Cloning and characterization of FKSG71, a novel gene encoding group
RL XIII secreted phospholipase A2."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Not known; does not seem to have catalytic activity.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AF39738; AK01739.1; -
CC MGD; MG1:1917086; Pla2g13.
CC InterPro; IPR00086; ER_target_S.
CC InterPro; IPR001211; PhospholipaseA2.
CC PROSITE; PS00119; PA2_ASP; FALSE NEG.
CC PROSITE; PS00118; PA2_HIS; FALSE NEG.
CC PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
CC Calcium; Signal.
CC SIGNAL 1 19 POTENTIAL.
CC CHAIN 20 195 GROUP XIII SECRETORY PHOSPHOLIPASE A2-
CC LIKE PROTEIN.
CC METAL 89 89 CALCIUM (VIA CARBONYL OXYGEN)
CC FT FT (BY SIMILARITY).
CC METAL 91 91 CALCIUM (VIA CARBONYL OXYGEN)

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FT METAL 93 93 (BY SIMILARITY).
FT CONFLICT 116 CALCIUM (VIA CARBONYL OXYGEN)
FT CONFLICT 116 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 195 AA; 21736 MW; 86F8E653BD08DA24 CRC64;

Query Match 88.8%; Score 946.5; DB 1; Length 195;
Best Local Similarity 88.7%; Pred. No. 2.5e-85;
Matches 173; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLASGFLVWLSLGGGLAQSDTSPTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60
DB 1 MKLASGFLVWLSLGGGLAQSDTSPTEESYSDWGLRHRLGSGFESVNSYFDSFLELLGK 60
QY 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIKPKATKCCNQLDVYD 120
DB 61 NGVCQYRCRYGKAPMPRGYKPOEPNGCGSYFLGLKVPESMDLGIKPKATKCCNQLDVYD 120
QY 121 TCGANKYRCDAKFRWCLXSLKSLGSLGFVSKVE-ACDSLVDTVFTNTVTLGCRPFMNS 179
DB 121 TCGANKYRCDAKFRWCLXSLKSLGSLGFVSKVE-ACDSLVDTVFTNTVTLGCRPFMNS 180
QY 180 QRAACICABEEKEEL 194
DB 181 QRAACICABEEKEEL 195

RESULT 3
PA2Z_MOUSE STANDARD; PRT; 192 AA.
AC Q9EP22; Q9QOR3; Q9CTU1; Q9D7L3; Q9EP21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Group XII secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase GXII) (GXII sPLA2).
GN PLA2G12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AKR;
RC MEDLINE=21264628; PubMed=11278438;
RA Ho I.C., Arm J.P., Bingham C.O. III, Choi A., Austen K.F.,
RA Glimcher L.H.;
RT "A novel group of phospholipase A2s preferentially expressed in type
RT 2 helper T cells."
RL J. Biol. Chem. 276:18321-18326(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RX Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RX Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RX Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RX Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RX Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
RX Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RX Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RX Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RX Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RX Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RX Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,
RX Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RX Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RX Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RX Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."

```

RL Nature 409:685-690 (2001).

[3]

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Olfactory epithelium;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-

CC acyl groups in 3-sn-phosphoglycerides.

CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

CC acylglycerophosphocholine + a fatty acid anion.

CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9EPR2-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9EPR2-2; Sequence=VSP_004509;

CC -1- SIMILARITY: Belongs to the phospholipase A2 family.

CC

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CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

CC EMBL; AY007381; AAG23336.1; -.

CC EMBL; AY007382; AAG23337.1; -.

CC EMBL; AK003183; -; NOT_ANNOTATED_CDS.

CC EMBL; AK009133; BAB26094.1; -.

CC EMBL; AK010011; BAB26641.1; -.

CC EMBL; AK010174; BAB26747.1; -.

CC EMBL; BC051117; AAB51117.1; -.

CC MGD; MGI:1913600; Pla2g12.

CC InterPro; IPR001211; PhospholipaseA2.

CC PROSITE; PS00119; PA2 ASP; FALSE NEG.

CC PROSITE; PS00118; PA2 HIS; 1.

CC Hydrolyase; Lipid degradation; Calcium; Signal; Alternative splicing.

CC SIGNAL 1 25 POTENTIAL

CC CHAIN 26 192 GROUP XII SECRETORY PHOSPHOLIPASE A2.

CC ACT_SITE 113 113 BY SIMILARITY.

CC ACT_SITE 128 128 BY SIMILARITY.

CC METAL 91 91 CALCIUM (VIA CARBONYL OXYGEN)

CC (BY SIMILARITY).

CC METAL 93 93 CALCIUM (VIA CARBONYL OXYGEN)

CC (BY SIMILARITY).

CC METAL 95 95 CALCIUM (VIA CARBONYL OXYGEN)

CC (BY SIMILARITY).

CC METAL 114 114 CALCIUM (BY SIMILARITY).

CC METAL 114 114 MVTPRPAPSPALLLLATARGQSDQDTWRATLKTI

CC VARSPLIC 1 73 RNIGHKIDTYLNAALDLGGEDGLQYKCSDG -> MKDHY

CC SFGPKYWEPAFPVCGSGTEEBELRIGR (in isoform

CC

FT FT 2).

FT CONFLICT 11 11 /FTId=VSP_004509.

FT CONFLICT 173 173 S -> G (IN REF. 1).

FT CONFLICT 192 AA; 21319 MW; 670ACE8F6AB6FCA2 CRC64; P -> H (IN REF. 2; BAB26094).

SO SEQUENCE

Query Match 43.8%; Score 467; DB 1; Length 192;

Best Local Similarity 43.9%; Pred. No. 1.7e-38;

Matches 83; Conservative 43; Mismatches 49; Indels 14; Gaps 3;

QY 8 LVIVLSGGGLAQSDSPDTEESYDW--GLRHLSGFESVNSYFDSFLBLGGKGVQC 65

Db 16 LLLLLATARGQEQDT-----TWRATLKIRNGIHKIDTYLNAALDLGGEDGLQC 67

QY 66 YRCRYGKAPMPRGYKPOEENCGSGVFLGLKVPESMDLGPAMTKCCNQDLVCYDTGCGAN 125

Db 68 YKCSDSGKPVPRGYKPSFNGGSGPLFGV----HLNIGIPSLTKCCNQDRCVETCKS 123

QY 126 KYRCDAKFRWCLXISGDLKRSKVFVSKVBPACDLSLVDTVFTVNTVTLGCRPFMSQRAACI 185

Db 124 KNDCEBEFYCLSKICRDVQKTLGLSQNVQACETTVELLFDVHLGCKEYLDQRAACW 183

QY 186 CAEEKEEL 194

Db 184 CRYEEKTDL 192

RESULT 4

PA2Y_HUMAN STANDARD; PRT; 189 AA.

ID PA2Y_HUMAN Q9EPR2; Q9EPR289;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Group XII secretory phospholipase A2 precursor (EC 3.1.1.4)

DE (Phosphatidylcholine 2-acylhydrolase GXII) (GXII SPLA2).

GN PLA2G12 OR FKSG38.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Metazoa; Chordata; Craniata; Hominidae; Homo.

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RP SEQUENCE FROM N.A., CHARACTERIZATION, AND MASS SPECTROMETRY.

RX MEDLINE=20568226; PubMed=11031251;

RX Gelb M.H., Valentini E., Ghomashchi F., Lazdunski M., Lambeau G.;

RT "Cloning and recombinant expression of a structurally novel human

RT secreted phospholipase A2.";

RT J. Biol. Chem. 275:39823-39826 (2000).

RL [2]

RP SEQUENCE FROM N.A.

RA Wang Y.-G., Gong L.;

RT "Identification of FKSG38, a novel gene located on human chromosome

RT 4q25.";

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94333817; PubMed=7520013;
RA Auchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;
RT "Cloning, sequence comparison and in vivo expression of the gene
encoding rat P-selectin.";
RL Gene 145:251-255(1994).
CC -!- FUNCTION: Ca(2+)-dependent receptor for myeloid cells that binds
CC to carbohydrates on neutrophils and monocytes. Mediates the
CC interaction of activated endothelial cells or platelets with
CC leukocytes. The ligand recognized is sialyl-Lewis X.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined: spleen,
CC lung, brain, liver, heart, kidney, thymus and small intestine.
CC -!- INDUCTION: By acute inflammation (probable).
CC -!- SIMILARITY: Belongs to the selectin/LECAM family.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 8 Sushi (SCR) domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L23088; AAA60325.1; -;
CC PIR; I53821; I53821.
CC RSP; P16109; IFSB.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR002396; Selectin.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 8.
CC PRINTS; PR00343; SELECTIN.
CC SMART; SM00032; CCP; 8.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS50026; EGF_3; 1.
CC Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate.
FT SIGNAL 1 41
FT CHAIN 42 768
FT DOMAIN 42 709
FT TRANSMEM 710 733
FT DOMAIN 734 768
FT DOMAIN 158 195
FT DOMAIN 159 195
FT DOMAIN 199 258
FT DOMAIN 261 320
FT DOMAIN 323 382
FT DOMAIN 385 444
FT DOMAIN 447 506
FT DOMAIN 509 568
FT DOMAIN 579 638
FT DOMAIN 641 700
FT DISULFID 60 158
FT DISULFID 131 150
FT DISULFID 168 183
FT DISULFID 185 194
FT DISULFID 200 244
FT DISULFID 230 257
FT DISULFID 262 306

FT DISULFID 292 319 BY SIMILARITY.
FT DISULFID 324 368 BY SIMILARITY.
FT DISULFID 354 381 BY SIMILARITY.
FT DISULFID 386 430 BY SIMILARITY.
FT DISULFID 416 443 BY SIMILARITY.
FT DISULFID 448 492 BY SIMILARITY.
FT DISULFID 478 505 BY SIMILARITY.
FT DISULFID 510 554 BY SIMILARITY.
FT DISULFID 540 567 BY SIMILARITY.
FT DISULFID 580 624 BY SIMILARITY.
FT DISULFID 610 637 BY SIMILARITY.
FT DISULFID 642 686 BY SIMILARITY.
FT DISULFID 672 699 BY SIMILARITY.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 654 654 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 661 661 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 745 745 S-palmitoyl cysteine (By similarity).
FT SITE 756 759 ENDOCYTOSIS SIGNAL (PROBABLE).
SQ SEQUENCE 768 AA; 83517 MW; 26FD78A5F3F1316 CRC64;
Query Match 8.2%; Score 87; DB 1; Length 768;
Best Local Similarity 26.4%; Pred. No. 1.1;
Matches 37; Conservative 9; Mismatches 42; Indels 52; Gaps 8;
QY 38 HLKGSFE-----SYNSYFDSFLELLGKNGVCQYRCYKAPMRPGYKPOEPNGCGS 90
Db 525 VHGGEPSVGSTCHFSCEE-----ELGSRNVECTVSGWSAPPTCKG----- 569
QY 91 YFLGLKVPESMDLGIPTAMT-----KCNQLD-----VCYDTC-----GANKYRCD 130
Db 570 -VTSLEVP---SVRCPALTPGQGTMSCHRHLESFGNTTCYFGCKTGTFLRGANSLRCG 625
QY 131 AKFRW-----CLXSICSDL 144
Db 626 ASQWTAVTPVCRVAKCSEL 645
RESULT 7
ID_FBL4_CRIGR STANDARD; PRT; 443 AA.
AC 055056;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
DE (Fibulin-4) (FBLN-4) (H411 protein).
GN EFEMP2 OR FBLN4.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Heine H., Delude R.L., Monks B., Golenbock D.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC      EMBL; AF046870; AAC03101.1; -.
CC      HSSP; P00736; IAP0.
CC      InterPro; IPR000152; Asx_hydroxyl_S.
CC      InterPro; IPR001861; EGF_Ca.
CC      InterPro; IPR006209; EGF_like.
CC      InterPro; IPR001491; Thrbomodulin.
CC      Pfam; PF00008; EGF; 4.
CC      PRINTS; PR00907; THRBOMODULN.
CC      SMART; SM00179; EGF_CA; 4.
CC      PROSITE; PS00010; ASX_HYDROXYL; 4.
CC      PROSITE; PS00022; EGF_1; FALSE_NEG.
CC      PROSITE; PS01186; EGF_2; 4.
CC      PROSITE; PS00026; EGF_3; 4.
CC      PROSITE; PS01187; EGF_CA; 6.
CC      Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
KW      SIGNAL
FT      CHAIN   1 25
FT      SIGNAL   26 443
FT      DOMAIN   36 81
FT      DOMAIN   123 163
FT      DOMAIN   164 202
FT      DOMAIN   203 242
FT      DOMAIN   243 282
FT      DOMAIN   283 328
FT      DOMAIN   329 368
FT      DISULFID 127 140
FT      DISULFID 134 149
FT      DISULFID 151 162
FT      DISULFID 168 177
FT      DISULFID 173 186
FT      DISULFID 188 201
FT      DISULFID 207 217
FT      DISULFID 213 226
FT      DISULFID 228 241
FT      DISULFID 247 258
FT      DISULFID 254 267
FT      DISULFID 269 281
FT      DISULFID 287 300
FT      DISULFID 294 309
FT      DISULFID 315 327
FT      CARBOHYD 198 198
FT      CARBOHYD 394 394
FT      SEQUENCE 443 AA; 49432 MW; 0BCFE5D7323D9E5F CRC64;
Query Match      8.1%; Score 86.5; DB 1; Length 443;
Best Local Similarity 22.2%; Pred. No. 0.64;
Matches 54; Conservative 19; Mismatches 71; Indels 99; Gaps 16;
QY      6 GFVLAV-----LSGGGLAQSDTSPDTEESYSD---WGL--RHLR-----GSF 43
DB      10 GSULLWALLLLGASQPDSPEPDSYCTECTDGYEWDADSQCHRDVNECLTPEACKGEM 69
QY      44 ESNVSYFDSFLELLGGKNGVQCVR-----RYGKAMP-----RFGYKP 82
DB      70 KCINHY-----GG-----YLCLPSAAVINDLHGEGPPPPVPAQHPNCPGYPEP 115
QY      83 QEPNGGSGYFLGLKVPESMDLGIPTMYTC-----CNQLDVCYDTCGANKYR-----C--- 129
DB      116 DEQESC-----VDVDECAQALHDCRFSDCHNLPGSYQCTCPDGYRKVGPECVDI 165
QY      130 -DAKFRWCLXISCDLKRSL-----GF-----VSKVEACD---SLVDVTFTVNTWL 171
DB      166 DECRYRYCQHR-CVNLPFSFRCQCEPQFGLQPNNRSCVDVNECDMGAPCQRCFNSYGTG 224
QY      172 GCR 174
DB      225 LCR 227
RESULT 8
Y083_NPVOP

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ID      Y083_NPVOP      STANDARD;      PRT;      819 AA.
AC      O10336;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Hypothetical 91.1 kDa protein (ORF86).
OS      Orygia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
OC      Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC      Nucleopolyhedrovirus.
OX      NCBI_TaxID=164623;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97271300; PubMed=9126251;
RA      Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA      Rohmann G.F.;
RT      "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
RT      polyhedrosis virus genome.";
RL      Virology 229:381-399(1997).
CC      -!- SIMILARITY: Contains 2 chitin-binding type-2 domains.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).


EMBL; U75930; AAC59085.1; -.  

InterPro; IPR002557; Chitin_bind_PerA.  

Pfam; PF01607; CBM 14; 1.  

SMART; SM00494; ChIBD2; 1.  

PROSITE; PS50940; CHIT_BIND_II; 2.  

Hypothetical protein; Chitin-binding; Repeat.  

SIGNAL 1 25 POTENTIAL.  

FT CHAIN 26 819 HYPOTHETICAL 91.1 KDA PROTEIN.  

FT DOMAIN 150 230 CHITIN-BINDING TYPE-2 1.  

FT DOMAIN 223 281 CHITIN-BINDING TYPE-2 2.  

FT SEQUENCE 819 AA; 91067 MW; 108942AFA0A8F925A CRC64;



Query Match      8.1%; Score 86.5; DB 1; Length 819;  

Best Local Similarity 24.7%; Pred. No. 1.3;  

Matches 45; Conservative 22; Mismatches 62; Indels 53; Gaps 9;



QY      46 VNSYF-----DSLELLGGKNGV--CQYRCYRGKAMPKPGYKQEPNGCGSYFLGLKV 97  

DB      234 VIAYFPETURVNEFVECRGKGVVARCPDQVFDRLMTCTVQTHPCAFNGAGHTYI--- 289  

QY      98 PESMDLIGIPAMTKCCNQLDVCYDTC-----GAN-KYRCDAKFRWCLXISCDLKRSLG-- 149  

DB      290 --TADIGDAQFFKCLNDREAQLITCINRVGADGQVACSGDAR-----CADLPDGTGRL 341  

QY      150 -----FVSKVEACDS-----LVDTFTVNTWILGCPFPNNSQBAACI 185  

DB      342 MHTHTDDTFEYVSGQTICDNYNVNVISSIECDTGNVLENKLFVNKFTLGAQ-FPREVLDAVG 400  

QY      186 CA 187  

DB      401 CA 402



RESULT 9  

WN1B_MOUSE  

ID      WN1B_MOUSE      STANDARD;      PRT;      389 AA.  

AC      P48614; P70702;  

DT      01-FEB-1996 (Rel. 33, Created)  

DT      01-FEB-1996 (Rel. 33, Last sequence update)  

DT      10-OCT-2003 (Rel. 42, Last annotation update)  

DE      Wnt-10b protein precursor (Wnt-12).  

GN      WNT10B OR WNT-10B OR WNT10 OR WNT12.  

OS      Mus musculus (Mouse).  

OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.


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| | |
|-----------------------|--|
| Query Match | 7.9%; Score 84.5; DB 1; Length 389; |
| Best Local Similarity | 22.0%; Pred. No. 0.86; |
| Matches | 29; Conservative 15; Mismatches 41; Indels 47; Gaps 5; |

| | | | |
|----|-----|--|-----|
| QY | 59 | GKNGVCQYRCRYGKAMPR-----PGYKQPEPNGCGSY | 91 |
| Db | 251 | GTSGSQQFTCWRAAPEFAIGAALRERLSRAITFDTHNRNSGAFQRLRPRLSGELVY | 310 |
| QY | 92 | FLGLKVPESMD---LGIPAMT-KCCNQLDVCYDTGCA-----NKYRCDAKF | 133 |
| Db | 311 | F-EKSPDFCERDPTUGSPGTRACNKUSSLRLLDGGSLCCGRGHNVLRQTRVERCHCRF | 368 |
| QY | 134 | RWCLXSICSLDK 145 | |
| Db | 369 | HWCCYVLCDECK 380 | |

| | | | | | | |
|-------------------|--|-----------------------------------|-----------|------|-----|-----|
| ID | ITB1 | MOUSE | STANDARD; | PRT; | 798 | AA. |
| AC | P09055; | | | | | |
| DT | 01-NOV-1988 | (Rel. 09, Created) | | | | |
| DT | 01-NOV-1988 | (Rel. 09, Last sequence update) | | | | |
| DT | 15-MAR-2004 | (Rel. 43, Last annotation update) | | | | |
| DE | Integrin beta-1 precursor (Fibronectin receptor beta subunit) | | | | | |
| DE | (CD29 antigen) (Integrin VLA-4 beta subunit). | | | | | |
| GN | ITGB1. | | | | | |
| OS | Mus musculus (Mouse). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | |
| NCBI_TaxID=10090; | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | STRAIN=BALB/c; | | | | | |
| RC | MEDLINE=89005707; PubMed=3262537; | | | | | |
| RA | Tominaga S.; | | | | | |
| RT | "Murine mRNA for the beta-subunit of integrin is increased in | | | | | |
| RT | BALB/c-3T3 cells entering the G1 phase from the G0 state."; | | | | | |
| RL | FEBS Lett. 238:315-319(1988). | | | | | |
| RN | [2] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | STRAIN=C57BL/6; TissuE=Brain; | | | | | |
| RC | MEDLINE=22388257; PubMed=12477932; | | | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | | | |
| RA | Klausner R.D., Collins F.S., Wegner L., Shennan C.M., Schuler G.D., | | | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | | | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | | | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., | | | | | |
| RA | Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | | | | |
| RA | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | | | |
| RA | Fahney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., | | | | | |
| RA | Whiting M., Madan A., Young A.C., Shvetchenko Y., Bouffard G.G., | | | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | | | | |
| RA | Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., | | | | | |
| RA | Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; | | | | | |
| RT | "Generation and initial analysis of more than 15,000 full-length | | | | | |
| RT | human and mouse cDNA sequences"; | | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | | | |
| RN | [3] | | | | | |
| RP | SEQUENCE OF 2-798 FROM N.A. | | | | | |
| RC | STRAIN=BALB/c; | | | | | |
| RC | MEDLINE=89235580; PubMed=2523953; | | | | | |
| RA | Holers V.M., Ruff T.G., Parks D.L., McDonald J.A., Ballard L.L., | | | | | |
| RA | Brown E.J.; | | | | | |
| RT | "Molecular cloning of a murine fibronectin receptor and its | | | | | |
| RT | expression during inflammation. Expression of VLA-5 is increased in | | | | | |
| RT | activated peritoneal macrophages in a manner discordant from major | | | | | |

RT histocompatibility complex class II.;

RL J. Exp. Med. 169:1589-1605 (1989).

CC -!- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-12/BETA-1 ARE RECEPTORS FOR VITRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF VITRONECTIN. INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1 ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR FOR VCAM1 AND RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-E-I IN CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLININ AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A WIDE ARRAY OF LIGANDS.

CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-1 associates with either alpha-1, alpha-2, alpha-3, alpha-4, alpha-5, alpha-6, alpha-7, alpha-8, alpha-9, alpha-10, alpha-11 or alpha-V. Interacts with FLNA and FLNB (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the integrin beta chain family.

CC -!- SIMILARITY: Contains 2 VWFA-like domains.

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DR EMBL; Y00769; CAA68738.1; -.

DR EMBL; BC050906; AAH50906.1; -.

DR EMBL; X15202; CAA33272.1; -.

DR PIR; PL0104; IJMSPB.

DR PIR; S01659; S01659.

DR HSP; P05106; IJVB2.

DR MGD; MGI:96610; Itgbl.

DR GO; GO:0005886; C:plasma membrane; IDA.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR002369; Integrin B.

DR InterPro; IPR001169; Integrin_beta_C.

DR InterPro; IPR003659; Plectin-like.

DR InterPro; IPR002035; VWF A.

DR Pfam; PF00362; integrin_B; 1.

DR ProDom; PD001811; IntegrinB.

DR PRINTS; PR01186; INTEGRINB.

DR SMART; SM00187; INB; 1.

DR SMART; SM00423; PSI; 1.

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS00243; INTEGRIN_BETA; 3.

DR PROSITE; PS00022; EGF_1; UNKNOWN 2.

KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;

KW Repeat; Signal; Phosphorylation.

FT SIGNAL 1 20

FT CHAIN 21 798 INTEGRIN BETA-1.

FT DOMAIN 21 728 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 729 751 POTENTIAL.

FT DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 140 378 VWFA-LIKE.

FT DOMAIN 466 635 4 CYSTEINE-RICH TANDEM REPEATS.

FT REPEAT 466 515 I.

FT REPEAT 516 559 III.

FT REPEAT 560 598 III.

FT REPEAT 599 635 IV.

FT DISULFID 27 464 BY SIMILARITY.

FT DISULFID 35 45 BY SIMILARITY.

FT DISULFID 38 75 BY SIMILARITY.

FT DISULFID 48 64 BY SIMILARITY.

FT DISULFID 207 213 BY SIMILARITY.

FT DISULFID 261 301 BY SIMILARITY.

FT DISULFID 401 415 BY SIMILARITY.

FT DISULFID 435 691 BY SIMILARITY.

FT DISULFID 462 466 BY SIMILARITY.

FT DISULFID 477 489 BY SIMILARITY.

FT DISULFID 486 525 BY SIMILARITY.

FT DISULFID 491 500 BY SIMILARITY.

FT DISULFID 502 516 BY SIMILARITY.

FT DISULFID 531 536 BY SIMILARITY.

FT DISULFID 533 568 BY SIMILARITY.

FT DISULFID 538 553 BY SIMILARITY.

FT DISULFID 555 560 BY SIMILARITY.

FT DISULFID 574 579 BY SIMILARITY.

FT DISULFID 576 607 BY SIMILARITY.

FT DISULFID 581 590 BY SIMILARITY.

FT DISULFID 592 599 BY SIMILARITY.

FT DISULFID 613 618 BY SIMILARITY.

FT DISULFID 615 661 BY SIMILARITY.

FT DISULFID 620 630 BY SIMILARITY.

FT DISULFID 633 636 BY SIMILARITY.

FT DISULFID 640 649 BY SIMILARITY.

FT DISULFID 646 723 BY SIMILARITY.

FT DISULFID 665 699 BY SIMILARITY.

FT MOD RES 783 783 PHOSPHORYLATION (BY SIMILARITY).

FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 363 363 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 417 417 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 520 520 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 584 584 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 669 669 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 385 385 E -> P (IN REF. 3).

FT CONFLICT 392 392 G -> A (IN REF. 3).

FT CONFLICT 443 445 IXI -> HSKL (IN REF. 3).

SQ SEQUENCE 798 AA; 88231 MW; 267888F70A168B56 CRC64;

Query Match 7.9%; Score 84; DB 1; Length 798;

Best Local Similarity 26.8%; Pred. No. 2.2;

Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;

QY 26 DTEESYSDWGLHRLGSP-ESVNSYFDSFLLELLGGKNGVCQYRCRYGKAPMPFGYKPOE 84

Db 543 NTNEIYS-----GKFCEDNFNCDNSNGLCGGNGVC--RCRVCE-----560

QY 85 PNGCGSYFLGLKVPESMDLG--IPAMTKCNQLDVCYDTGCGANKVRC-DAKFRWCLXSTC 141

Db 581 ---CYPNYTGSAQDCSLDTGCPCLASNGQICNGRGIC--ECGACK--CTDPKQ---GPTC 630

QY 142 SLDKRSGLGFVSKVEACDSIVDTVFNTVTLTGCRPPNWSQRAACICAE 189

Db 631 ETCQTCGLGVCAEHKEC-----VQCRAF-NKGEKKDTCAQE 664

RESULT 11

FBL4_HUMAN

ID FBL4_HUMAN STANDARD; PRT; 443 AA.

AC Q95967; O75967;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE EGF-containing fibulin-like extracellular matrix protein 2 precursor (Fibulin-4) (FBLN-4) (UPH1 protein) (UNQ200/PRO226).

GN EFEMP2 OR FBLN4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RX TISSUE=Melanoma;
RA MEDLINE=20068041; PubMed=10601734;
RT Giltay R., Timpi R., Koska G.;
RL "Sequence, recombinant expression and tissue localization of two novel
RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
RN Matrix Biol. 18:469-480(1999).
RN [2]
RN SEQUENCE FROM N.A.
RA Zemel R., Shaul Y.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=20435063; PubMed=10982184;
RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;
RL "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
RT from the multiple retinopathy critical region on 11q13.";
RN Hum. Genet. 106:66-72(2000).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RL "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ132819; CAAL0791.2; -

DR EMBL; AF093119; AAC62108.1; -.
DR EMBL; AF109121; AAF65188.1; -.
DR EMBL; AY358899; AAG9258.1; -.
DR EMBL; BC010456; AAH10456.1; -.
DR HSSP; P35555; IEMN.
DR Genew; HGNC:3219; EFEMP2.
DR MIM; 604633; -.
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001491; Thrbomodulin.
DR Pfam; PF00008; EGF; 4.
DR PRINTS; PRO0907; THRBOMODULN.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL
FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT DOMAIN 36 81 MATRIX PROTEIN 2.
FT DOMAIN 123 163 EGF-LIKE 1, DIVERGENT.
FT DOMAIN 164 202 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 203 242 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 243 282 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 283 328 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 127 140 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 134 149 BY SIMILARITY.
FT DISULFID 151 162 BY SIMILARITY.
FT DISULFID 168 177 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 188 201 BY SIMILARITY.
FT DISULFID 207 217 BY SIMILARITY.
FT DISULFID 213 226 BY SIMILARITY.
FT DISULFID 228 241 BY SIMILARITY.
FT DISULFID 247 258 BY SIMILARITY.
FT DISULFID 254 267 BY SIMILARITY.
FT DISULFID 269 281 BY SIMILARITY.
FT DISULFID 287 300 BY SIMILARITY.
FT DISULFID 294 309 BY SIMILARITY.
FT DISULFID 315 327 BY SIMILARITY.
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 5 5 A -> T (IN REF. 1).
FT CONFLICT 44 51 EMDPDSQH -> TOTAN (IN REF. 2).
FT CONFLICT 103 111 ACHNPCCP -> VNTQPLET (IN REF. 2).
FT CONFLICT 294 294 C -> W (IN REF. 2).
FT CONFLICT 354 356 RSV -> AER (IN REF. 2).
FT CONFLICT 355 355 S -> R (IN REF. 3).
FT SEQUENCE 443 AA; 49391 MW; 9E9AC2393780D3B8 CRC64;
SQ
Query Match 7.8%; Score 83.5; DB 1; Length 443;
Best Local Similarity 21.9%; Pred. No. 1.2;
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;
QY 6 GFVLW-----LSLGGGLAQSDTSPDTEESYSD---W--GLRHRL-----GSF 43
DB 10 GSLLWALLLLLSGASPDSEPDSTYCTDGYEWDPSQHCVDYNECLTPEACKGEM 69
QY 44 ESNVSFDSFLELLGKNGVCQYRC-----RYGKAPMP-----RPGYKP 82
DB 70 KCHNY-----GG-----YLCUPRSAVINDLHGEGPPPPVPAQHNPCCPGYEP 115
QY 83 QEPNGCGSYFLGLKVPESMDLGIPTAMTKC-----CNQLDVCYDTGANKYR-----C--- 129
DB 116 DDQDSC-----VDVDECAQALHDCRPDSQDCHNLPGSYQCTCPDGYRKIGPECVDI 165
QY 130 -DAKFRWCLXSGISDLKRSI-----GF-----VSKVEACD---SLVDVTFTVNTWTL 171

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Db 166 DBCRYRYQHR-CVNLPGSFRQCCEPGLGPNRSCVDVNECDMGAPCEQRCFNSYCTG 224
QY 172 GCR 174
Db 225 LCR 227

RESULT 12
UREL_YEREN
ID UREL_YEREN STANDARD; PRT; 571 AA.
AC P31494;
DT 01-JUL-1993 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
GN URE C OR YBUC.
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2635 / Serotype O:3;
RX MEDLINE=94320783; PubMed=8045421;
RA de Koning-Ward T.P., Ward A.C., Robins-Browne R.M.;
RT "Characterisation of the urease-encoding gene complex of Yersinia
enterocolitica.";
RL Gene 145:25-32(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=6471/76 / Serotype O:3;
RX MEDLINE=93273501; PubMed=8500886;
RA Skurnik M., Batsford S., Mertz A.K.H., Schiltz E., Toivanen P.;
RT "The putative arthritogenic cationic 19-kilodalton antigen of
Yersinia enterocolitica is a urease beta-subunit.";
RL Infect. Immun. 61:2498-2504(1993).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
CC -!- PTM: Lys-221 is carbamylated. The carbamoyl group provides the
ligands for the two nickel ions (By similarity).
CC -!- SIMILARITY: Belongs to the urease family.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; L24101; AAA50996.1; -
DR EMBL; Z18865; CAA79316.1; -
DR FIR; S36028; S36028.
DR HSSP; P18314; 1FWF.
DR MEROPS; M38.UNW; -.
DR InterPro; IPR006680; Amidohydro 1.
DR InterPro; IPR005848; Pept M38 urease.
DR InterPro; IPR008295; Urease_alpha.
DR Pfam; PF01979; Amidohydro_1; 1.
DR Pfam; PF00449; urease; 1.
DR FIRSF; FIRSF001226; Urease_alpha; 1.
DR PRINTS; PR01752; UREASE.
DR PROSITE; PS00145; UREASE_2; 1.
DR PROSITE; PS01120; UREASE_1; 1.
KW Hydrolase; Metal-binding; Nickel.
FT INIT_MET 0 0 BY SIMILARITY.
FT METAL 138 138 NICKEL 2 (BY SIMILARITY).
FT METAL 140 140 NICKEL 2 (BY SIMILARITY).
FT METAL 221 221 NICKEL 1 AND 2 (BY SIMILARITY).
FT METAL 250 250 NICKEL 1 (BY SIMILARITY).
FT METAL 276 276 NICKEL 1 (BY SIMILARITY).
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FT METAL 364 364 NICKEL 2 (BY SIMILARITY).
FT ACT SITE 324 324 BY SIMILARITY.
FT CONFLICT 29 30 IE -> MQ (IN REF. 2).
FT CONFLICT 66 66 V -> GY (IN REF. 2).
FT CONFLICT 68 82 DLVITNTIVDARLG -> EFSHNQRHYCCSPFR
(IN REF. 2).
FT CONFLICT 96 96 A -> V (IN REF. 2).
FT CONFLICT 114 114 M -> L (IN REF. 2).
FT CONFLICT 137 137 S -> T (IN REF. 2).
FT CONFLICT 405 405 L -> V (IN REF. 2).
FT CONFLICT 440 440 D -> V (IN REF. 2).
SQ SEQUENCE 571 AA; 60952 MW; 99C7944554FB58EA CRC64;

Query Match 7.8%; Score 83.5; DB 1; Length 571;
Best Local Similarity 25.8%; Pred. No. 1.7;
Matches 31; Conservative 17; Mismatches 49; Indels 23; Gaps 5;

QY 15 GGLAQSDTSPDTEESYSDWGLRHRLRGSFES--VNSYFDSLELLGGKNGVCQYRCRYGK 72
Db 160 GGGIGPTDGTNGTTVTGPMNIRQMLRSVEGLPVN-----VGILGKNS-----YGR 206
QY 73 APMRP-----GYKQPEPNGCGSYFL--GLKVPESMDLGPAMTKCCNQLDVCYDTGCA 124
Db 207 GPLELQAIAGVVGKVEDWGTATNALRHSURMAEDMDIQSVHTDSLNECGVEDTIDA 266

RESULT 13
WN1B HUMAN
ID WN1B HUMAN STANDARD; PRT; 389 AA.
AC O00744; O00747; O8WZ97;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wnt-10b protein precursor (Wnt-12).
GN WNT10B OR WNT12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97430838; PubMed=9284937;
RA Hardman G., Kastelein R.A., Bazan J.F.;
RT "Isolation, characterization and chromosomal localization of human
WNT10B.";
RL Cytogenet. Cell Genet. 77:278-282(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21570122; PubMed=11713588;
RA Saitoh T., Kirikoshi H., Mine T., Katoh M.;
RT "Proto-oncogene WNT10B is up-regulated by tumor necrosis factor alpha
in human gastric cancer cell line MKN45.";
RL Int. J. Oncol. 19:1187-1192(2001).
RN [3]
RP SEQUENCE OF 45-347 FROM N.A.
RX TISSUE=Fetal brain;
RX MEDLINE=97236668; PubMed=9121776;
RA Bui T.D., Rankin J., Smith K., Huguet E.L., Ruben S., Strachan T.,
RA Harris A.L., Lindsay S.;
RT "A novel human Wnt gene, WNT10B, maps to 12q13 and is expressed in
human breast carcinomas.";
RL Oncogene 14:1249-1253(1997).
RN [4]
RP SEQUENCE OF 253-368 FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=98110581; PubMed=9441749;
RA Bergstein I., Eisenberg L.M., Bhalarao J., Jenkins N.A.,
RA Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
RT "Isolation of two novel WNT genes, WNT14 and WNT15, one of which
(WNT15) is closely linked to WNT3 on human chromosome 17q21.";
RL Genomics 46:450-458(1997).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors. Probable developmental protein. May be a
```

CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters (By similarity). Possibly secreted and associates with the
CC extracellular matrix.
CC -!- SUBCELLULAR LOCATION: DETECTED IN MOST ADULT TISSUES. HIGHEST LEVELS
CC -!- TISSUE SPECIFICITY: DETECTED IN MOST ADULT TISSUES. HIGHEST LEVELS
CC WERE FOUND IN HEART AND SKELETAL MUSCLE. LOW LEVELS ARE FOUND IN
CC BRAIN.
CC -!- DEVELOPMENTAL STAGE: INFANT BRAIN HAS HIGHER LEVELS OF WNT10B THAN
CC ADULT BRAIN.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC
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CC
CC EMBL; U81787; AAB51695.1; -
CC EMBL; AB070724; BAB72181.1; -
CC EMBL; X97057; CAA65769.1; -
CC EMBL; AF028700; AAC39549.1; -
CC Genew; HGNC:12775; WNT10B.
CC MIM; 601906; -
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR005816; Wnt_grthfactor.
CC Pfam; PF00110; wnt; 1.
CC PRINTS; PR01349; WNTPROTEIN.
CC SMART; SM00097; WNT1; 1.
CC PROSITE; PS00246; WNT1; 1.
CC Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
KW SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 389 WNT-10B PROTEIN.
FT CARBOHYD 93 93 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 60 60 G -> D (IN REF. 1).
FT CONFLICT 149 149 K -> R (IN REF. 3).
FT CONFLICT 295 295 P -> S (IN REF. 3).
FT CONFLICT 311 311 F -> L (IN REF. 3).
SQ SEQUENCE 389 AA; 43000 MW; F973F2CA0DB115EF CRC64;

Query Match 7.7%; Score 82.5; DB 1; Length 389;
Best Local Similarity 21.2%; Pred. No. 1.4;
Matches 28; Conservative 16; Mismatches 41; Indels 47; Gaps 5;

QY 59 GRNGVQYRCRYGKAMP- - - - -PGYKQPNPGCGSY 91
Db 251 GTSGCQFKTCWRAEPEFRAVGAALRRLGRAIFIDTHNRNSGAFQPLRPRLSGELVY 310

QY 92 FLGLKVPESMD- - - - -LGIPAMT-KCCNQLDVCYDTGCA- - - - -NKYRCDAKF 133
Db 311 F- - - - -EKGFPCERDPTMGSPGTRACNKTSLRLDGGCLCCGSHNVLRQTRVERCHCRF 368

QY 134 RWCLXSICSLK 145
Db 369 HWCYVLCDECK 380

RESULT 14
URE1 YERPS STANDARD; PRT; 571 AA.
AC P52313;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
GN UREAC.
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;

RN SEQUENCE FROM N.A.
RP STRAIN=IP 2777;
RC MEDLINE=97270511; PubMed=9125594;
RA Riott B., Berche P., Simonet M.;
RT "Urease is not involved in the virulence of Yersinia
RT pseudotuberculosis in mice."
RL Infect. Immun. 65:1985-1990(1997).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
CC -!- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).
CC -!- PTM: Lys-221 is carbamylated. The carbamoyl group provides the
CC ligands for the two nickel ions (By similarity).
CC -!- SIMILARITY: Belongs to the urease family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U40842; AAB7854.1; -
CC HSP; P18314; 1FWF.
CC MEROPS; M38.UNW; -
CC InterPro; IPR006680; Amidohydro 1.
CC InterPro; IPR005848; Pept_M38_urease.
CC InterPro; IPR008295; Urease_alpha.
CC Pfam; PF01979; Amidohydro_1; 1.
CC Pfam; PF00449; urease; 1.
CC PRINTS; PIRSF001226; Urease_alpha; 1.
CC PRINTS; PR01752; UREASE.
CC PROSITE; PS00145; UREASE_2; 1.
CC PROSITE; PS01200; UREASE_1; 1.
CC Hydrolase; Metal-binding; Nickel.
KW INIT MET 0 0 BY SIMILARITY.
FT METAL 138 138 NICKEL 2 (BY SIMILARITY).
FT METAL 140 140 NICKEL 2 (BY SIMILARITY).
FT METAL 221 221 NICKEL 1 AND 2 (BY SIMILARITY).
FT METAL 250 250 NICKEL 1 (BY SIMILARITY).
FT METAL 276 276 NICKEL 1 (BY SIMILARITY).
FT METAL 364 364 NICKEL 2 (BY SIMILARITY).
FT ACT SITE 324 324 BY SIMILARITY.
SQ SEQUENCE 571 AA; 60874 MW; 88B6056FA16F89CC CRC64;

Query Match 7.6%; Score 81.5; DB 1; Length 571;
Best Local Similarity 25.0%; Pred. No. 2.6;
Matches 30; Conservative 18; Mismatches 49; Indels 23; Gaps 5;

QY 15 GGGIAQSDTSPTESYSDWGLRHLRGSFES--VNSYFDSFLELLGGKNGVCQYRCRYGK 72
Db 160 GGGIGTDTGNTSVTPGPWNIRQLRSIEGLPVN-----VGILKGNS-----YGR 206

QY 73 AMPRP-----GYKQPNPGCGSYFL--GLKVPESMDLGIPTAMTKCCNQLDVCYDTGCA 124
Db 207 GPLLEQAIAGVGVYKVHEDWGATANALRALHRAHMADEVDIQSVVHTDSLNECGYVEITIDA 266

RESULT 15
IBP2_RAT STANDARD; PRT; 304 AA.
AC P12843;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 2 precursor (IGFBP-2)
DE (IBP-2) (IGF-binding protein 2) (BRL-IP).
GN IGFBP2 OR IGFBP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89174801; PubMed=2538475;
RA Brown A.L., Chiarlotti L., Orlovski C.C., Mehlman T., Burgers W.H.,
RA Ackerman E.J., Bruni C.B., Reckler M.M.;
RT "Nucleotide sequence and expression of a cDNA clone encoding a fetal
RT rat binding protein for insulin-like growth factors.";
RL J. Biol. Chem. 264:5148-5154(1989).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90014825; PubMed=2477691;
RA Margot J.B., Binkert C., Mary J.-L., Landwehr J., Heinrich G.,
RA Schwanter J.;
RT "A low molecular weight insulin-like growth factor binding protein
RT from rat: cDNA cloning and tissue distribution of its messenger
RT RNA.";
RL Mol. Endocrinol. 3:1053-1060(1989).
RN
RP SEQUENCE OF 38-68.
RX MEDLINE=86278218; PubMed=2426267;
RA Mottola C., Macdonald R.G., Brackett J.L., Mole J.E., Anderson J.K.,
RA Czech M.P.;
RT "Purification and amino-terminal sequence of an insulin-like growth
RT factor-binding protein secreted by rat liver BRL-3A cells.";
RL J. Biol. Chem. 261:11180-11188(1986).
RN
RP SEQUENCE OF 35-64.
RC TISSUE=Sera;
RX MEDLINE=89073708; PubMed=2480123;
RA Shimonaka M., Schroeder R., Shimasaki S., Ling N.;
RT "Identification of a novel binding protein for insulin-like growth
RT factors in adult rat serum.";
RL Biochem. Biophys. Res. Commun. 165:189-195(1989).
RN
RP SEQUENCE OF 178-204.
RX MEDLINE=89076308; PubMed=2974285;
RA Wang J.F., Hampton B., Mehlman T., Burgess W.H., Rechler M.M.;
RT "Isolation of a biologically active fragment from the carboxy
RT terminus of the fetal rat binding protein for insulin-like growth
RT factors.";
RL Biochem. Biophys. Res. Commun. 157:718-726(1988).
CC -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs
CC and have been shown to either inhibit or stimulate the growth
CC promoting effects of the IGFs on cell culture. They alter the
CC interaction of IGFs with their cell surface receptors.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: Binds IGF-II more than IGF-I.
CC -!- SIMILARITY: Contains 1 IGFBP domain.
CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
CC
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CC
CC EMBL; J04486; AAA0829.1; -;
CC EMBL; M56559; -; NOT_ANNOTATED_CDS.
CC EMBL; M31672; AAA1381.1; -;
CC PIR; A33274; A33274.
CC HSSP; P24593; IBOE.
CC InterPro; IPR009030; Grow fac recep.
CC InterPro; IPR008867; Insl_gro_fac_pr.
CC InterPro; IPR000716; Thyroglobulin_1.
CC Pfam; PF00219; IGFBP; 1.
CC Pfam; PF00086; thyroglobulin_1; 1.
CC PIRSF; PIRSF001969; IGFBP1-6; 1.
CC SMART; SM00121; IB; 1.
CC SMART; SM00211; TY; 1.
CC PROSITE; PS00222; IGF_BINDING; 1.

DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 34
FT CHAIN 35 304 INSULIN-LIKE GROWTH FACTOR BINDING
FT DOMAIN 236 285 PROTEIN 2.
FT SITE 280 282 THYROGLOBULIN TYPE-I.
FT CONFLICT 298 298 CELL ATTACHMENT SITE.
SQ SEQUENCE 304 AA; 32883 MW; 8558B7E2C915348F CRC64;
Query Match 7.6%; Score 80.5; DB 1; Length 304;
Best Local Similarity 22.5%; Pred. No. 1.6;
Matches 39; Conservative 25; Mismatches 60; Indels 49; Gaps 9;
QY 26 DTEESYSDWGLRHLSGSPESVNSYFDSLELLGGKNGVCQYRCYKAKMPRPYK--- 81
DB 129 DSEDDHSEGG---VENHVDGTMNMGSSA-----GRKP-PKSGMKELAV 170
QY 82 -----POEPNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCGANKYRCDAKFR 134
DB 171 PREKYNEQHRQMGKGAHLSLEPKKL-RPPPARTPCQQLDQVLERISTMLPDD---R 226
QY 135 WCLXICSDLKRSLSGVSKVEACDSLVDTVFNVTWL-GCRPFMNSQRAACIC 186
DB 227 GPLEHLYS-----LHFPNCDK-----HGLYNLKQCKMSLNGQGEWC 264
Search completed: May 17, 2004, 10:42:46
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:39:44 ; Search time 45 Seconds
(without alignment)
1360.234 Million cell updates/sec

Title: US-10-621-401-145
Perfect score: 1066
Sequence: 1 MKLAGFLVWLSLGGGLAQ.....PFMNSQRAACICAEKEEL 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp archea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp virus:*
16: sp bacteriaph:*
17: sp archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 949.5 | 89.1 | 195 | 11 Q8VC81 | Q8VC81 mus musculus |
| 2 | 677 | 63.5 | 180 | 13 Q7ZTY1 | Q7ZTY1 brachydanio |
| 3 | 465 | 43.6 | 205 | 11 Q8BMX2 | Q8BMX2 mus musculus |
| 4 | 441.5 | 41.4 | 242 | 13 Q7ZV17 | Q7ZV17 brachydanio |
| 5 | 230 | 21.6 | 230 | 5 Q9VUV6 | Q9VUV6 drosophila |
| 6 | 186 | 17.4 | 114 | 5 Q8XC7 | Q8XC7 drosophila |
| 7 | 96.5 | 9.1 | 254 | 5 Q9BL06 | Q9BL06 caenorhabdi |
| 8 | 87.5 | 8.2 | 1037 | 2 Q8VLQ3 | Q8VLQ3 alteromonas |
| 9 | 86.5 | 8.1 | 281 | 5 Q8SXC6 | Q8SXC6 drosophila |
| 10 | 86.5 | 8.1 | 342 | 5 Q9W410 | Q9W410 drosophila |
| 11 | 85.5 | 8.0 | 1054 | 16 Q87HX4 | Q87HX4 vibrio para |
| 12 | 84.5 | 7.9 | 117 | 5 Q8M050 | Q8M050 caenorhabdi |
| 13 | 84 | 7.9 | 798 | 11 Q8BTU0 | Q8BTU0 mus musculus |
| 14 | 83.5 | 7.8 | 443 | 4 Q96TF5 | Q96TF5 homo sapien |
| 15 | 83.5 | 7.8 | 854 | 16 Q87HH8 | Q87HH8 vibrio para |
| 16 | 83.5 | 7.8 | 1053 | 2 Q8KRL3 | Q8KRL3 vibrio harv |

| | | | | | |
|----|------|-----|------|-----------|---------------------|
| 17 | 82 | 7.7 | 1070 | 16 Q8D7E1 | Q8D7E1 vibrio vuln |
| 18 | 82 | 7.7 | 1289 | 5 Q86AC3 | Q86AC3 dictyosteli |
| 19 | 81 | 7.6 | 2192 | 5 Q01768 | Q01768 caenorhabdi |
| 20 | 80.5 | 7.6 | 443 | 11 Q9JN06 | Q9JN06 mus musculus |
| 21 | 80.5 | 7.6 | 1051 | 16 Q9KLP3 | Q9KLP3 vibrio chol |
| 22 | 80.5 | 7.6 | 1526 | 10 Q7XW03 | Q7XW03 oryza sativ |
| 23 | 80 | 7.5 | 414 | 10 Q9SH19 | Q9SH19 arabidopsis |
| 24 | 80 | 7.5 | 553 | 12 Q83536 | Q83536 measles vir |
| 25 | 80 | 7.5 | 553 | 12 Q83533 | Q83533 measles vir |
| 26 | 80 | 7.5 | 632 | 5 Q9VFN3 | Q9VFN3 drosophila |
| 27 | 80 | 7.5 | 822 | 11 Q62287 | Q62287 mus musculu |
| 28 | 79.5 | 7.5 | 317 | 6 Q97599 | Q97599 bos taurus |
| 29 | 79.5 | 7.5 | 443 | 4 Q9H3D5 | Q9H3D5 homo sapien |
| 30 | 79.5 | 7.5 | 1241 | 5 Q9U144 | Q9U144 leishmania |
| 31 | 79.5 | 7.5 | 1704 | 5 Q94446 | Q94446 chironomus |
| 32 | 79 | 7.4 | 419 | 5 Q810M3 | Q810M3 giardia lam |
| 33 | 79 | 7.4 | 446 | 11 Q8BV23 | Q8BV23 mus musculu |
| 34 | 79 | 7.4 | 504 | 11 Q8BZT7 | Q8BZT7 mus musculu |
| 35 | 79 | 7.4 | 621 | 2 Q9F486 | Q9F486 alteromonas |
| 36 | 79 | 7.4 | 621 | 2 Q53401 | Q53401 alteromonas |
| 37 | 79 | 7.4 | 692 | 16 Q8A6D1 | Q8A6D1 bacteroides |
| 38 | 79 | 7.4 | 712 | 5 Q20323 | Q20323 caenorhabdi |
| 39 | 78.5 | 7.4 | 1821 | 4 Q14767 | Q14767 homo sapien |
| 40 | 78.5 | 7.4 | 2189 | 5 Q9BI05 | Q9BI05 eimeria ten |
| 41 | 78 | 7.3 | 177 | 5 Q8IML0 | Q8IML0 drosophila |
| 42 | 78 | 7.3 | 411 | 16 Q8CXW6 | Q8CXW6 escherichia |
| 43 | 78 | 7.3 | 638 | 4 Q8N8H6 | Q8N8H6 homo sapien |
| 44 | 78 | 7.3 | 710 | 11 Q91VP4 | Q91VP4 mus musculu |
| 45 | 78 | 7.3 | 710 | 11 Q61898 | Q61898 mus musculu |

ALIGNMENTS

RESULT 1

Q8VC81
ID Q8VC81 PRELIMINARY; PRT; 195 AA.
AC Q8VC81;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-VAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RIKEN cDNA 2010002E04 gene.
GN 2010002E04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021592; AAH21592.1; -;
DR MGD; MGI:1917086; 2010002E04RIK.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR000886; ER_target_S.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 195 AA; 21722 MW; 83A8E65ED08DA24 CRC64;

Query Match 89.1%; Score 949.5; DB 11; Length 195;
Best Local Similarity 89.2%; Pred. No. 5.8e-96;
Matches 174; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

| | | | | |
|----|----|--|--|--|
| QY | 1 | MKLAGFLVWLSLGGGLAQSDTSPDTEESYSDWGLRHRLRGFSFVSNSYDFLELLGK 60 | | |
| Db | 1 | MKLCGFFLLWLGVLGNLAQSDPSPKEESYSDWGLRQLRGFSFVSNSYVDSFMELGK 60 | | |
| QY | 61 | NGVCQYRCRYGKAPMPRPGYKQEPNGCCSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120 | | |
| Db | 61 | NGVCQYRCRYGKAPMPRPGYKQEPNGCCSYFLGLKVPESMDLGIPTAMTKCCNQLDVCYD 120 | | |

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QY 121 TCGANKYCDKFRWCLXSIKSDIKRSLGFSKYVE-ACDSLVDVTVTNTLGCRRPFMNSQRAACICAEKEEEL 179
DB 121 TCGANKYCDKFRWCLXSIKSDIKRSLGFSVNEFAACDSLADTDTVTNTLGCRRPFMNS 180

QY 180 QRAACICAEKEEEL 194
DB 181 QRAACICAEKEEEL 195

RESULT 2
Q7ZTV1
ID Q7ZTV1 PRELIMINARY; PRT; 180 AA.
AC Q7ZTV1
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to phospholipase A2, group XIII.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23288257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whitton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Body;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC052113; AAHS2113.1; --
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR000886; ER target S.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00014; ER_TARGET, 1.
SQ SEQUENCE 180 AA; 19975 MW; F44C2620E690A601 CRC64;

Query Match 63.5%; Score 677; DB 13; Length 180;
Best Local Similarity 67.6%; Pred. No. 4.3e-66;
Matches 115; Conservative 23; Mismatches 26; Indels 6; Gaps 2;

QY 27 TRESY--SWGLRHURGSPESVNSYFDSFLELLGKNGVCQYRCYRGKAPMPRGYKQOE 84
DB 15 TRESDDDDWGFSGIRGSLQSYNGYFDSFLELLGKNGVCQYRCYRGKAPMPRGYQMS 74

QY 85 PNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCGANKYCDKFRWCLXSIKSD 144
DB 75 PDGCSISLLGQ-----FDMGVFAMTKCCNQLDVCYDTCCGANKYCDKFRWCLXSIKSD 130

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QY 145 KRSGLGFSKYVEACDSLVDVTVTNTLGCRRPFMNSQRAACICAEKEEEL 194
DB 131 KXSLGLMSKYVEACETFDATNTNTLGCRRPFMNGQASCYCEGEKDEL 180

RESULT 3
Q8BMX2
ID Q8BMX2 PRELIMINARY; PRT; 205 AA.
AC Q8BMX2
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Group XII-1 phospholipase A2 (Fragment).
GN PLA2G12 OR 2310004B05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK012414; BAC25368.1; --
DR MGB; MGI:1913600; Pla2g12.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS, 1.
FT NON TER 1
SQ SEQUENCE 205 AA; 22495 MW; 040FRAEEF01DE691 CRC64;

Query Match 43.6%; Score 465; DB 11; Length 205;
Best Local Similarity 43.9%; Pred. No. 9.5e-43;
Matches 83; Conservative 42; Mismatches 50; Indels 14; Gaps 3;

QY 8 LVLMISLGGHQAQSDTSDPTESYSDW--GLRHURGSPESVNSYFDSFLELLGKNGVCQ 65
DB 29 LLLLLATARGOEQDT-----PDWRATLKTIRNGIHKIDTYLNAALDLGGEDGLCQ 80

QY 66 YRCYRGKAPMPRGYKQEPNGCGSYFLGLKVPESMDLIGIPAMTKCCNQLDVCYDTCCG 125
DB 81 YKSDSGSKPVRGYKSPNGCGSPFGV---HLNIGIFSLTKCCNQHRCVETCKS 136

QY 126 KYRCDKFRWCLXSIKSDIKRSLGFSKYVEACDSLVDVTVTNTLGCRRPFMNSQRAACI 185
DB 137 KNDCEDEFQYCLSKICRDVQKTGLSQNVQACETTVLLFSDVHLGCKPYLDQSRAACW 196

QY 186 CAEEKEEL 194
DB 197 CRYEKTDL 205

RESULT 4
Q7ZV17
ID Q7ZV17 PRELIMINARY; PRT; 242 AA.
AC Q7ZV17
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Body;
RA Strauberg B.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046040; AAH46040.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hypothetical protein.
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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Man K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
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RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
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RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Takahashi K.;
RT "Cloning of Drosophila group XIV secreted phospholipase A2."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003529; AAF49567.2; -.
DR EMBL; AF349541; AAK30169.1; -.
DR FlyBase; Fgn0036545; GXIVePLA2.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
DR SEQUENCE 230 AA; 25952 MW; 925882C6D32F3466 CRC64;
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Query Match 21.6%; Score 230; DB 5; Length 230;
 Best Local Similarity 30.8%; Pred. No. 6.9e-17;
 Matches 60; Conservative 31; Mismatches 50; Indels 54; Gaps 11;
 30 SYSDWG---LRHURGS-----FESVNSYFDSFLELLGKNGVCQ 65

19 AYSGSGSTTVHLRDAIIAAEAFGVDVFNKLVLRKPTVHEVDAVD-----EN--CI 72
66 YRCRYGKAPRPPG-----YKQBPNGSGSYFLGLKVPESMDLGIIPA--MTKCC 112
73 YQC-----PAPDIGPAPRAVQNFYTP-TADGGGS--LGLRI--STDY-LPAKEMETCC 121
113 NQLDVVCYDTCGANKYRCDAKFRWCLXISCDLKRSLGFSVKVEACDSLVDVFNVTWTLG 172
122 NDHDCYDTCNSDKELCDLDFKRLCYKYSYKSIASDLMMKGCCKAAAKMLFTGTLTLG 181
173 CRPFNWSQRAACICA 187
182 CRSYLDQQRSYCYCA 196
RESULT 6
Q8SX7 PRELIMINARY; PRT; 114 AA.
ID Q8SX7
AC Q8SX7
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE GH07145P (CGI7035-PB).
GN CXIVSPLA2 OR CGI7035.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan B., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherzer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman M.R., Bouck J., Brokstein P., Brotter P.,
RA Borkova D., Botchan M.R., Boutin B.F., Boudreau N., Boudreau P.,
RA Burtis K.C., Busam D.A., Butler H.C., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Durbin K.J., Gabor G.L., Gabor G.L., Gabor G.L., Gabor G.L.,
RA Glisic A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Fittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
[3]
SEQUENCE FROM N.A.
RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan B.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
RP Mirra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., De Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094681; AAM11034.1; -;
DR EMBL; AE003529; AAN11772.1; -;
DR FlyBase; PBgn0036545; GXIVPLA2.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2 HTS; 1.
SQ SEQUENCE 114 AA; 13155 MW; 020303F23839E262 CRC64;
Query Match 17.4%; Score 186; DB 5; Length 114;
Best Local Similarity 37.5%; Pred. No. 2e-12;
Matches 30; Conservative 16; Mismatches 34; Indels 0; Gaps 0;
QY 108 MTKCNQDVCYDTCGANKYRCDAKFRWCLXISCDLKRSLGFSVKVEACDSLVDVFNVT 167
DB 1 METCNDHDCYDTCNSDKELCDLDFKRLCYKYSYKSIASDLMMKGCCKAAAKMLFTG 60
QY 168 VMTLGRPFNWSQRAACICA 187
DB 61 TITLGRSYLDQQRSYCYCA 80
RESULT 7
ID Q9BL06 PRELIMINARY; PRT; 254 AA.
AC Q9BL06;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

HSP; P15445; 1A3D.
DR FlyBase; FBgn029720; CG3009.
DR GO; GO:005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; F:lipo catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR InterPro; IPR008774; phospholip_A2.
DR Pfam; PF05826; Phospholip_A2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00118; PA_2_HIS; 1.
SQ SEQUENCE 342 AA; 38426 MW; 6SEB9A337ABEF4878 CRC64;

Query Match 8.1%; Score 86.5; DB 5; Length 281;
Best Local Similarity 25.6%; Pred.No. 0.5;
Matches 30; Conservative 15; Mismatches 49; Indels 23; Gaps 4;

QY 51 DSFLELLGGKNGVCVRCRYGKAPMPRGYPKGPEPGCGSYFLGLKVPSMDLGPAM-T 109
: : : : :
16 ESMVEL-----EEVCRQGSGYGHEFRGLGIYFGTKWCP---GTAAATSYDDLGAHARE 68

DB 110 KCNQLDVDCYTCCANKYR-----CDAKFRWLXSIICSDLKRSIGLV 151
: : : : :
69 RCCEHDMCPDVNLVGECRRGLNCRGTFTRSHCHDDCFARFCRLQAANTETANGAI 125

RESULT 10
ID Q9W410 PRELIMINARY; PRT; 342 AA.

AC Q9W410;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CG3009 protein.
GN Drosophila melanogaster (fruit fly).
OS Drosophila melanogaster (Insecta); Insecta; Hexapoda; Arthropoda; Metazoa; Eukaryota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Sutton G.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle J., Andrews-Pfannkuch C., Baldwin D.,
RA Abriel J.F.M., Agbayani A., An H.-J., Bayraktaroglu U., Beasley E.M.,
RA Ballwey R.M., Basu A., Baxendale J., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Beeson K.V., Benos P.V., Berman B.P., Brodeur P., Brotter P.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Buttner P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pabloes B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garq N.S., Galbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulop D., Lai X.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svarksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserma D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster";
RT Science 287:2185-2195 (2000).
DR EMBL; AF003431; AAF45972.1; -.

Query Match 8.0%; Score 85.5; DB 16; Length 1054;
Best Local Similarity 24.2%; Pred.No. 3.2;

HSP; P15445; 1A3D.
DR FlyBase; FBgn029720; CG3009.
DR GO; GO:005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; F:lipo catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR InterPro; IPR008774; phospholip_A2.
DR Pfam; PF05826; Phospholip_A2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00118; PA_2_HIS; 1.
SQ SEQUENCE 342 AA; 38426 MW; 6SEB9A337ABEF4878 CRC64;

Query Match 8.1%; Score 86.5; DB 5; Length 342;
Best Local Similarity 25.6%; Pred.No. 0.63;
Matches 30; Conservative 15; Mismatches 49; Indels 23; Gaps 4;

QY 51 DSFLELLGGKNGVCVRCRYGKAPMPRGYPKGPEPGCGSYFLGLKVPSMDLGPAM-T 109
: : : : :
77 ESMVEL-----EEVCRQGSGYGHEFRGLGIYFGTKWCP---GTAAATSYDDLGAHARE 129

DB 110 KCNQLDVDCYTCCANKYR-----CDAKFRWLXSIICSDLKRSIGLV 151
: : : : :
130 RCCEHDMCPDVNLVGECRRGLNCRGTFTRSHCHDDCFARFCRLQAANTETANGAI 186

RESULT 11
ID Q87HX4 PRELIMINARY; PRT; 1054 AA.

AC Q87HX4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chitodextrinase.
GN VP0832.
OS Vibrio parahaemolyticus.
OC Bacateria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Tajima Y., Nakajima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."; Lancet 361:743-749 (2003).
RT EMBL; AP005086; BAC62175.1; --
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
DR GO; GO:0008246; F:carbohydrate binding; IEA.
DR GO; GO:0003887; F:dna-directed DNA polymerase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR GO; GO:0006260; P:dna replication; IEA.
DR InterPro; IPR003610; CBM 5 12.
DR InterPro; IPR006172; DNA_DOL_B.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR InterPro; IPR000437; Prok_lipoprot_S.
DR Pfam; PF02839; CBM 5 12; 2.
DR Pfam; PF00704; Glyco hydro 18; 1.
DR PROSITE; PS01095; CHITINASE 18; 1.
DR PROSITE; PS00116; DNA POLYMERASE B; 1.
DR PROSITE; PS00013; PROKARYOTIC LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 1054 AA; 111857 MW; 92EE689F138EBE7E CRC64;

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Matches 30; Conservative 19; Mismatches 36; Indels 39; Gaps 6;
Qy 14 LGGLASDTSPTDTE-----ESY-----SDWGLRLHRSFES-----VNSYFD 51
Db VGHNAALFDTKGDSBELAQWNVYGTAAAGIGYLTNDWAYHYFRGSMAGRINIGVYYTR 631
Qy 52 SFLELLGGKNGVCQVRCRYGKAPW-----RPGYKQPQPNCGSYFLGLK-----VPES 100
Db 632 GWQGVGTGDNGL-----WGRAALPNQACQPGTGEGEKNNGCNGAIGIDNNWHDLDPQG 685
Qy 101 MDLG 104
Db 686 REMG 689

RESULT 12
QBMQ50
ID QBMQ50 PRELIMINARY; PRT; 117 AA.
AC QBMQ50;
DT 01-MAR-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein F44B9.10.
GN F44B9.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Watson R.;
RT "Genome sequencing of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fulton L.;
RT "The sequence of C. elegans cosmid F44B9.";
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; L23648; AAM48524.1; -.
DR WormPep; F44B9.10; CE30988.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 13359 MW; 51A3EB08F7BBE4C7 CRC64;

Query Match 7.9%; Score 84.5; DB 5; Length 117;
Best Local Similarity 25.2%; Pred. No. 0.28;
Matches 27; Conservative 13; Mismatches 48; Indels 19; Gaps 3;

Qy 63 VCQVRCRYGKAPWPRPGYK-----POEPNGCGSYFLGLKV-----PESMDLGIPTAMKCCNQ 114
Db 1 MCNVRCIYAVLFIVFLSKYIAQLVPEFRFCGSGSISTSIYSTSSVFCQIQLNQCCMY 60
Qy 115 LDVCYDTGCGANKYRCDAKFRWCLXSCDLKRSLSGFSKVEACDSLV 161
Db 61 HDLCYAGCTLPQMECDNQFCECLATISN-----PFCQSIV 96

RESULT 13
QBMQ50
ID QBMQ50 PRELIMINARY; PRT; 798 AA.
AC QBMQ50;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Integrin beta 1.
GN ITGB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK088729; BAC40532.1; -.
DR MGI; MGI:96610; Itgb1.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF00362; Integrin_B; 1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
DR PROSITE; PS00022; EGF_1_2.
DR PROSITE; PS00243; INTEGRIN_BETA; 3.
SQ SEQUENCE 798 AA; 88246 MW; 8867DC4D55DBE898 CRC64;

Query Match 7.9%; Score 84; DB 11; Length 798;
Best Local Similarity 26.8%; Pred. No. 3.3;
Matches 45; Conservative 16; Mismatches 57; Indels 50; Gaps 11;

Qy 26 DTEESYSDWGLRLHRSF-ESVNSVDFDSFLELLGGKNGVCQVRCRYGKAPWPRPGYKPOE 84
Db 543 NTNEIYS-----GKFCEDNFNCDNRNGICGNGVC--RCRVCE-----S80
Qy 85 PNGCGSYFLGLKVPESSMDLG--IPAMTKCCNQLDVCYDTGCGANKYRC-DAKFRWCLXSC 141
Db 581 ---CYPNTYGSACDCSLDTGPGCLASNGQICNGRGIC--ECGACK--CTDPKFO--GPTC 630
Qy 142 SLDKRSLSGFSKVEACDSILVDTVNTVTLGCRPFMNSORACICAE 189
Db 631 ETCQTCGLGVCAEHKEC-----VQCRAP-NKGEKDTCAQE 664

RESULT 14
Q96TF5
ID Q96TF5 PRELIMINARY; PRT; 443 AA.
AC Q96TF5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mutant p53 binding protein 1 (MBP1).
GN MBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanka S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
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RA Tanaka S., Sugimachi K., Sugimachi K.;
RT "Human mutant p53 binding protein (MBP1).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030655; BAA92880.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; F:blood coagulation; IEA.
DR InterPro; IPR001582; Asx_Hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF; 4.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 443 AA; 49421 MW; 9CE175F4F388A56D CRC64;

Query Match 7.8%; Score 83.5; DB 4; Length 443;
Best Local Similarity 21.8%; Pred. No. 1.8;
Matches 53; Conservative 21; Mismatches 70; Indels 99; Gaps 16;

QY 6 GFIVLW-----LSLGGGLAQSPTSPTESYSD--W--GLRHLR-----GSP 43
DB 10 GSLLLWALLLLLSASPDSEEDPSYTECHDGYEWDPSQCRDVECLTIPEACKGEM 69

QY 44 ESVNSYFDSFLELLGKNGVCQYRC-----RYGKAMP-----RPGYKP 82
DB 70 KCIHY-----GG-----YLCLPSAAVINDLHGEPPPPVPPAQHENPCPPGYEP 115

QY 83 QEPNGCGSYFLGLKVPESMDLIGIPAMTKC-----CNQLDVCYDTGANKYR-----C--- 129
DB 116 DDQDSC-----VDVDECAQALHDCRPSQDCHNLPFGSYQCTCPDGYRKIGPECVDI 165

QY 130 -DAKFRWCLXSTCSPLKESL-----GF-----VSKVEACD---SLVDIVENTVWTL 171
DB 166 DECRYRYCOHR-CVNLPGSFRQCQPPGFQGLGNPNRSCVDVNECDMGAPCEQCFSNYGTF 224

QY 172 GCR 174
DB 225 LCR 227

RESULT 15
Q87HH8 PRELIMINARY; PRT; 854 AA.
AC Q87HH8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Nitrite reductase (NAD(P)H), large subunit.
GN VPA0987.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62330.1;
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001327; FAD_pyr_redox.

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DR InterPro; IPR007419; Fer2_BFD.
DR InterPro; IPR006066; Nir_Si.
DR InterPro; IPR006067; Nir_Sir_4Fe4S.
DR InterPro; IPR005117; Nir_sir_fer.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF04324; fer2_BFD; 1.
DR Pfam; PF01077; Nir_Sir; 1.
DR Pfam; PF03460; Nir_Sir_fer; 1.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; ENDRDTASEI.
DR PRINTS; PR00397; SIROHAEM.
DR PROSITE; PS00365; NIR_SIR; 1.
KW Complete proteome.
SQ SEQUENCE 854 AA; 93571 MW; D0EC68D3CF42ABB6 CRC64;

Query Match 7.8%; Score 83.5; DB 16; Length 854;
Best Local Similarity 26.7%; Pred. No. 4.1;
Matches 32; Conservative 11; Mismatches 48; Indels 29; Gaps 5;

QY 19 AQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGKNGVCQYRCRYGKAMPERP 78
DB 509 AQKDDLPETWRKLLDAG-----FETGQAYAKA---LRMAKTCVGSTWCRYG----- 651

QY 79 GYKPPQEPNGCGSY-----FLGLKVPESMDLIGIPAMTKCC-----NQLDVCYDTGANKYRC 129
DB 652 ---VQDSVGLGSYIENRYKGIPTPHKMKFGVSGCTRECAEAQKGLGIATDAGWNNMYC 708

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Search completed: May 17, 2004, 10:43:44

Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:44:24 ; Search time 60 Seconds
(without alignments)
913.570 Million cell updates/sec

Title: US-10-621-401-145
Perfect score: 194
Sequence: 1 MKLASGLVWLSLGGGLAQ.....PFMNSQRAACICABEEKEEL 194

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 193 | 99.5 | 194 | 6 | ADA57403 Human sec |
| 2 | 193 | 99.5 | 194 | 6 | ADA41278 Human sec |
| 3 | 193 | 99.5 | 194 | 6 | ABO13978 Novel hum |
| 4 | 193 | 99.5 | 194 | 6 | ABR48024 Human sec |
| 5 | 193 | 99.5 | 195 | 2 | AAY27572 Human sec |
| 6 | 137 | 70.6 | 194 | 5 | ADP62920 Human pol |
| 7 | 137 | 70.6 | 194 | 6 | ADA56921 Human sec |
| 8 | 137 | 70.6 | 194 | 6 | ADA40769 Human sec |
| 9 | 137 | 70.6 | 194 | 6 | ADA47739 Human sec |
| 10 | 137 | 70.6 | 194 | 6 | ADA08422 Novel pro |
| 11 | 8 | 4.1 | 439 | 6 | ADM67608 Photornab |
| 12 | 7 | 3.6 | 19 | 2 | AAR99965 Clahl12 B- |
| 13 | 7 | 3.6 | 23 | 2 | AAR72674 Cladospor |
| 14 | 7 | 3.6 | 34 | 2 | ADB48041 Novel hum |
| 15 | 7 | 3.6 | 35 | 2 | AAR60689 M.kandler |
| 16 | 7 | 3.6 | 87 | 4 | AAU17876 Novel hum |
| 17 | 7 | 3.6 | 88 | 3 | AAU14126 Bordetell |
| 18 | 7 | 3.6 | 104 | 4 | ABG29089 Novel hum |
| 19 | 7 | 3.6 | 110 | 2 | AAR99961 Cladospor |
| 20 | 7 | 3.6 | 110 | 6 | ABR53058 Protein s |
| 21 | 7 | 3.6 | 111 | 2 | AAR72669 Cladospor |
| 22 | 7 | 3.6 | 144 | 2 | AAY29625 Human +5 |
| 23 | 7 | 3.6 | 144 | 3 | AAY49952 Human +5 |
| 24 | 7 | 3.6 | 171 | 3 | AAG42859 Arabidops |
| 25 | 7 | 3.6 | 171 | 3 | AAG15427 Arabidops |

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| 26 | 7 | 3.6 | 171 | 4 | ABG09375 | Abg09375 Novel hum |
| 27 | 7 | 3.6 | 172 | 4 | ABG19489 | Abg19489 Novel hum |
| 28 | 7 | 3.6 | 176 | 4 | AAU29035 | Aau29035 T. gondii |
| 29 | 7 | 3.6 | 176 | 4 | AAU25506 | Aau25506 T. gondii |
| 30 | 7 | 3.6 | 191 | 3 | AAU44335 | Aay44335 Arabidops |
| 31 | 7 | 3.6 | 191 | 3 | AAU15426 | Aag15426 Arabidops |
| 32 | 7 | 3.6 | 191 | 3 | AAU42858 | Aag42858 Arabidops |
| 33 | 7 | 3.6 | 191 | 5 | AAE25101 | Aae25101 Arabidops |
| 34 | 7 | 3.6 | 191 | 7 | AAE37930 | Aag37930 Human CGD |
| 35 | 7 | 3.6 | 202 | 4 | ABG29088 | Abg29088 Novel hum |
| 36 | 7 | 3.6 | 204 | 2 | AAW25770 | Aaw25770 Human hD5 |
| 37 | 7 | 3.6 | 204 | 2 | AAW54075 | Aaw54075 Human tum |
| 38 | 7 | 3.6 | 204 | 2 | AAU29626 | Aay29626 Human D53 |
| 39 | 7 | 3.6 | 204 | 2 | AAU29624 | Aay29624 Mouse D53 |
| 40 | 7 | 3.6 | 204 | 3 | AAU49953 | Aay49953 Mouse D53 |
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| 42 | 7 | 3.6 | 224 | 3 | ABR57054 | AbR57054 Human pro |
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| 46 | 7 | 3.6 | 288 | 5 | AAE15792 | Aae15792 Xenopus 1 |
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| 50 | 7 | 3.6 | 320 | 5 | AAO14857 | Aaol14857 Serratia |
| 51 | 7 | 3.6 | 320 | 5 | AAE29090 | Aae29090 Serratia |
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| 53 | 7 | 3.6 | 327 | 6 | ABR82856 | AbR82856 NIT relat |
| 54 | 7 | 3.6 | 327 | 6 | ABU38786 | Abu38786 Protein e |
| 55 | 7 | 3.6 | 339 | 6 | ABM68139 | Abm68139 Photornab |
| 56 | 7 | 3.6 | 343 | 2 | AAU77656 | Aay77656 Human zin |
| 57 | 7 | 3.6 | 347 | 2 | AAU20108 | Aay20108 B. burgdo |
| 58 | 7 | 3.6 | 359 | 2 | AAU00245 | Aay00245 Enterococ |
| 59 | 7 | 3.6 | 359 | 5 | ABP43464 | Abp43464 E faecal |
| 60 | 7 | 3.6 | 359 | 6 | ABU68492 | Abu68492 E. faecal |
| 61 | 7 | 3.6 | 359 | 6 | ABU13743 | Abu13743 Enterococ |
| 62 | 7 | 3.6 | 380 | 3 | AAU54208 | Aag54208 Arabidops |
| 63 | 7 | 3.6 | 380 | 3 | AAU08922 | Aag08922 Arabidops |
| 64 | 7 | 3.6 | 390 | 3 | AAU23655 | Aag23655 Arabidops |
| 65 | 7 | 3.6 | 390 | 3 | AAU46070 | Aag46070 Arabidops |
| 66 | 7 | 3.6 | 390 | 3 | AAU32484 | Aag32484 Arabidops |
| 67 | 7 | 3.6 | 396 | 2 | AAW55070 | Aaw55070 Streptoco |
| 68 | 7 | 3.6 | 396 | 5 | ABP54564 | Abp54564 S. pneumo |
| 69 | 7 | 3.6 | 396 | 5 | ADC45097 | Adc45097 S. pneumo |
| 70 | 7 | 3.6 | 397 | 3 | AAU08921 | Aag08921 Arabidops |
| 71 | 7 | 3.6 | 397 | 3 | AAU54207 | Aag54207 Arabidops |
| 72 | 7 | 3.6 | 418 | 3 | AAU46069 | Aag46069 Arabidops |
| 73 | 7 | 3.6 | 418 | 3 | AAU23654 | Aag23654 Arabidops |
| 74 | 7 | 3.6 | 418 | 3 | AAU32483 | Aag32483 Arabidops |
| 75 | 7 | 3.6 | 419 | 6 | ABU02394 | Abu02394 S. pneumo |
| 76 | 7 | 3.6 | 419 | 6 | ABU46234 | Abu46234 Protein e |
| 77 | 7 | 3.6 | 420 | 3 | AAU91669 | Aay91669 Streptoco |
| 78 | 7 | 3.6 | 420 | 3 | AAU91041 | Aay91041 Alysia ca |
| 79 | 7 | 3.6 | 434 | 5 | ABR78288 | AbR78288 Amino aci |
| 80 | 7 | 3.6 | 442 | 3 | AAU23653 | Aag23653 Arabidops |
| 81 | 7 | 3.6 | 442 | 3 | AAU46068 | Aag46068 Arabidops |
| 82 | 7 | 3.6 | 454 | 2 | AAU00135 | Aay00135 Enterococ |
| 83 | 7 | 3.6 | 454 | 5 | ABP43354 | Abp43354 E faecal |
| 84 | 7 | 3.6 | 454 | 6 | ABU8382 | Abu8382 E. faecal |
| 85 | 7 | 3.6 | 454 | 6 | ABU13633 | Abu13633 Enterococ |
| 86 | 7 | 3.6 | 456 | 6 | AAO16378 | Aaol16378 Murine pa |
| 87 | 7 | 3.6 | 464 | 3 | AAU68739 | Aay68739 Amino aci |
| 88 | 7 | 3.6 | 465 | 4 | AAU96333 | Aab96333 Putative |
| 89 | 7 | 3.6 | 476 | 3 | AAU91036 | Aay91036 Human car |
| 90 | 7 | 3.6 | 476 | 3 | AAU91037 | Aay91037 Rat carbo |
| 91 | 7 | 3.6 | 476 | 3 | AAU91040 | Aay91040 Murine ca |
| 92 | 7 | 3.6 | 476 | 4 | AAU23880 | Aam23880 Human EST |
| 93 | 7 | 3.6 | 476 | 5 | AAU84326 | Abu84326 Protein C |
| 94 | 7 | 3.6 | 476 | 5 | AAU84326 | Abu84326 Protein C |
| 95 | 7 | 3.6 | 476 | 5 | ABR78283 | AbR78283 Amino aci |
| 96 | 7 | 3.6 | 476 | 5 | ABR78283 | AbR78283 Amino aci |
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| 98 | 7 | 3.6 | 476 | 5 | ABR78287 | AbR78287 Amino aci |

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| 103 | 7 | 3.6 | 491 | 3 | AAG73399 | 176 | 6 | 3.1 | 7 | 5 | ABG77600 | 117 | 6 | ABG77600 | Targettin |
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| 110 | 7 | 3.6 | 516 | 3 | AAW59414 | 183 | 6 | 3.1 | 15 | 5 | ABG71130 | 124 | 6 | ABG71130 | SR protei |
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| 116 | 7 | 3.6 | 547 | 3 | AAW59412 | 189 | 6 | 3.1 | 16 | 6 | ABO06500 | 130 | 6 | ABO06500 | N-myristo |
| 117 | 7 | 3.6 | 547 | 3 | AAW59412 | 190 | 6 | 3.1 | 18 | 2 | AAW1838 | 131 | 6 | AAW1838 | A.alterna |
| 118 | 7 | 3.6 | 564 | 4 | ABW58909 | 191 | 6 | 3.1 | 20 | 4 | AAW20242 | 132 | 6 | AAW20242 | Peptide # |
| 119 | 7 | 3.6 | 649 | 2 | AAW70260 | 192 | 6 | 3.1 | 20 | 4 | AAW34342 | 133 | 6 | AAW34342 | Peptide # |
| 120 | 7 | 3.6 | 649 | 2 | AAW70259 | 193 | 6 | 3.1 | 20 | 4 | AAW24872 | 134 | 6 | AAW24872 | Protein # |
| 121 | 7 | 3.6 | 649 | 2 | AAW70259 | 194 | 6 | 3.1 | 20 | 4 | AAW74230 | 135 | 6 | AAW74230 | Human bon |
| 122 | 7 | 3.6 | 650 | 2 | AAW49107 | 195 | 6 | 3.1 | 20 | 4 | AAW74230 | 136 | 6 | AAW74230 | Human bon |
| 123 | 7 | 3.6 | 652 | 2 | AAW63808 | 196 | 6 | 3.1 | 20 | 4 | AAW61440 | 137 | 6 | AAW61440 | Human bra |
| 124 | 7 | 3.6 | 652 | 2 | AAW70499 | 197 | 6 | 3.1 | 20 | 4 | ABG56032 | 138 | 6 | ABG56032 | Human liv |
| 125 | 7 | 3.6 | 684 | 7 | ADC37562 | 198 | 6 | 3.1 | 20 | 5 | ABG44183 | 139 | 6 | ABG44183 | Human pep |
| 126 | 7 | 3.6 | 722 | 5 | ABG32998 | 199 | 6 | 3.1 | 22 | 2 | AAW34039 | 140 | 6 | AAW34039 | Neuropept |
| 127 | 7 | 3.6 | 759 | 2 | AAW41927 | 200 | 6 | 3.1 | 22 | 2 | AAW19545 | 141 | 6 | AAW19545 | Amino aci |
| 128 | 7 | 3.6 | 759 | 2 | AAW46593 | 201 | 6 | 3.1 | 25 | 4 | ABG52659 | 142 | 6 | ABG52659 | Human liv |
| 129 | 7 | 3.6 | 759 | 4 | AAW92754 | 202 | 6 | 3.1 | 25 | 5 | ABG40737 | 143 | 6 | ABG40737 | Human pep |
| 130 | 7 | 3.6 | 771 | 7 | ADC31519 | 203 | 6 | 3.1 | 29 | 4 | ABW51137 | 144 | 6 | ABW51137 | Human sec |
| 131 | 7 | 3.6 | 788 | 5 | AAW47977 | 204 | 6 | 3.1 | 29 | 4 | ABW50870 | 145 | 6 | ABW50870 | Human sec |
| 132 | 7 | 3.6 | 791 | 6 | ABO52988 | 205 | 6 | 3.1 | 29 | 4 | AAO09139 | 146 | 6 | AAO09139 | Human pol |
| 133 | 7 | 3.6 | 792 | 3 | AAW42779 | 206 | 6 | 3.1 | 29 | 6 | ABO45127 | 147 | 6 | ABO45127 | Novel hum |
| 134 | 7 | 3.6 | 816 | 5 | ABW33952 | 207 | 6 | 3.1 | 29 | 6 | ABO45394 | 148 | 6 | ABO45394 | Novel hum |
| 135 | 7 | 3.6 | 875 | 5 | ABP62960 | 208 | 6 | 3.1 | 29 | 7 | ABO26607 | 149 | 6 | ABO26607 | Protein a |
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| 138 | 7 | 3.6 | 894 | 6 | ABU13631 | 211 | 6 | 3.1 | 31 | 4 | ABW24634 | 152 | 6 | ABW24634 | Protein # |
| 139 | 7 | 3.6 | 913 | 4 | ABW62729 | 212 | 6 | 3.1 | 31 | 4 | AAW73660 | 153 | 6 | AAW73660 | Human bon |
| 140 | 7 | 3.6 | 913 | 4 | AAW00136 | 213 | 6 | 3.1 | 31 | 4 | AAO09252 | 154 | 6 | AAO09252 | Human pol |
| 141 | 7 | 3.6 | 962 | 2 | AAW00132 | 214 | 6 | 3.1 | 31 | 4 | AAW60966 | 155 | 6 | AAW60966 | Human bra |
| 142 | 7 | 3.6 | 962 | 2 | AAW00244 | 215 | 6 | 3.1 | 31 | 4 | ABG55395 | 156 | 6 | ABG55395 | Human liv |
| 143 | 7 | 3.6 | 962 | 2 | AAW00248 | 216 | 6 | 3.1 | 31 | 5 | ABG43532 | 157 | 6 | ABG43532 | Human pep |
| 144 | 7 | 3.6 | 962 | 2 | AAW00248 | 217 | 6 | 3.1 | 31 | 5 | ABG43532 | 158 | 6 | ABG43532 | Human pep |
| 145 | 7 | 3.6 | 962 | 2 | AAW00246 | 218 | 6 | 3.1 | 32 | 5 | ABP29426 | 159 | 6 | ABP29426 | Streptoco |
| 146 | 7 | 3.6 | 962 | 2 | AAW00134 | 219 | 6 | 3.1 | 32 | 5 | AAU97163 | 160 | 6 | AAU97163 | Human G-p |
| 147 | 7 | 3.6 | 962 | 5 | ABP43463 | 220 | 6 | 3.1 | 32 | 6 | ABO06471 | 161 | 6 | ABO06471 | Human G-p |
| 148 | 7 | 3.6 | 962 | 5 | ABP43463 | 221 | 6 | 3.1 | 32 | 7 | ABO33899 | 162 | 6 | ABO33899 | Anti-GPI- |
| 149 | 7 | 3.6 | 962 | 5 | ABP43467 | 222 | 6 | 3.1 | 32 | 7 | AAW87260 | 163 | 6 | AAW87260 | KEKE-moti |
| 150 | 7 | 3.6 | 962 | 5 | ABP43355 | 223 | 6 | 3.1 | 33 | 2 | AAW87260 | 164 | 6 | AAW87260 | KEKE-moti |
| 151 | 7 | 3.6 | 962 | 5 | ABP43353 | 224 | 6 | 3.1 | 34 | 4 | ABW41266 | 165 | 6 | ABW41266 | Peptide # |
| 152 | 7 | 3.6 | 962 | 5 | ABP43353 | 225 | 6 | 3.1 | 34 | 4 | AAW35051 | 166 | 6 | AAW35051 | Peptide # |
| 153 | 7 | 3.6 | 962 | 5 | ABP43351 | 226 | 6 | 3.1 | 34 | 4 | ABW35051 | 167 | 6 | ABW35051 | Peptide # |
| 154 | 7 | 3.6 | 962 | 6 | ABU88491 | 227 | 6 | 3.1 | 34 | 4 | ABW35051 | 168 | 6 | ABW35051 | Peptide # |
| 155 | 7 | 3.6 | 962 | 6 | ABU88379 | 228 | 6 | 3.1 | 34 | 4 | AAW74935 | 169 | 6 | AAW74935 | Human bon |
| 156 | 7 | 3.6 | 962 | 6 | ABU88383 | 229 | 6 | 3.1 | 34 | 4 | AAW62131 | 170 | 6 | AAW62131 | Human bra |
| 157 | 7 | 3.6 | 962 | 6 | ABU88439 | 230 | 6 | 3.1 | 34 | 4 | ABG56711 | 171 | 6 | ABG56711 | Human liv |
| 158 | 7 | 3.6 | 962 | 6 | ABU88495 | 231 | 6 | 3.1 | 34 | 5 | ABG44686 | 172 | 6 | ABG44686 | Human pep |
| 159 | 7 | 3.6 | 962 | 6 | ABU13634 | 232 | 6 | 3.1 | 36 | 3 | AAW56444 | 173 | 6 | AAW56444 | Human pro |
| 160 | 7 | 3.6 | 962 | 6 | ABU13746 | 233 | 6 | 3.1 | 37 | 3 | AAW54258 | 174 | 6 | AAW54258 | Insert of |
| 161 | 7 | 3.6 | 962 | 6 | ABU13630 | 234 | 6 | 3.1 | 41 | 4 | AAW15285 | 175 | 6 | AAW15285 | Peptide # |
| 162 | 7 | 3.6 | 962 | 6 | ABU13744 | 235 | 6 | 3.1 | 41 | 4 | AAW67463 | 176 | 6 | AAW67463 | Human bon |
| 163 | 7 | 3.6 | 962 | 6 | ABU13742 | 236 | 6 | 3.1 | 41 | 4 | AAW67463 | 177 | 6 | AAW67463 | Human bon |
| 164 | 7 | 3.6 | 962 | 6 | ABU13632 | 237 | 6 | 3.1 | 41 | 4 | AAW55070 | 178 | 6 | AAW55070 | Human rep |
| 165 | 7 | 3.6 | 1083 | 6 | ABW33704 | 238 | 6 | 3.1 | 44 | 4 | AAW94876 | 179 | 6 | AAW94876 | Human rep |
| 166 | 7 | 3.6 | 1137 | 4 | ABW63815 | 239 | 6 | 3.1 | 44 | 4 | AAW91250 | 180 | 6 | AAW91250 | Human imm |
| 167 | 7 | 3.6 | 1131 | 7 | ADDA6288 | 240 | 6 | 3.1 | 45 | 4 | AAW91250 | 181 | 6 | AAW91250 | Human imm |
| 168 | 7 | 3.6 | 1191 | 7 | ADE63058 | 241 | 6 | 3.1 | 46 | 4 | AAW90668 | 182 | 6 | AAW90668 | C Glutami |
| 169 | 7 | 3.6 | 1203 | 7 | ADW70304 | 242 | 6 | 3.1 | 46 | 4 | AAW90668 | 183 | 6 | AAW90668 | Human pep |
| 170 | 7 | 3.6 | 1209 | 5 | ABP73800 | 243 | 6 | 3.1 | 48 | 4 | AAW90668 | 184 | 6 | AAW90668 | Human pep |
| 171 | 7 | 3.6 | 1211 | 4 | ABB64663 | 244 | 6 | 3.1 | 49 | 4 | AAW91249 | 185 | 6 | AAW91249 | Human pol |

| | | | | | | | | | | | | | |
|-----|---|-----|----|---|----------|-----------|-----|---|-----|----|---|----------|-----------|
| 245 | 6 | 3.1 | 51 | 4 | ABG10137 | Novel hum | 318 | 6 | 3.1 | 64 | 4 | AAM67959 | Human bon |
| 246 | 6 | 3.1 | 51 | 4 | ABG26503 | Novel hum | 319 | 6 | 3.1 | 64 | 4 | AAM76223 | Human bon |
| 247 | 6 | 3.1 | 51 | 5 | ABP33067 | Human ORF | 320 | 6 | 3.1 | 64 | 4 | AAM63410 | Human bra |
| 248 | 6 | 3.1 | 52 | 4 | ABP33067 | Peptide # | 321 | 6 | 3.1 | 64 | 4 | AAM55577 | Human bra |
| 249 | 6 | 3.1 | 52 | 4 | ABP33067 | Peptide # | 322 | 6 | 3.1 | 64 | 4 | ABG57940 | Human liv |
| 250 | 6 | 3.1 | 52 | 4 | ABP33067 | Peptide # | 323 | 6 | 3.1 | 64 | 4 | ABG49601 | Human liv |
| 251 | 6 | 3.1 | 52 | 4 | ABP33067 | Peptide # | 324 | 6 | 3.1 | 64 | 4 | AAM03513 | Peptide # |
| 252 | 6 | 3.1 | 52 | 4 | ABP33067 | Peptide # | 325 | 6 | 3.1 | 64 | 5 | ABG37495 | Human pep |
| 253 | 6 | 3.1 | 52 | 4 | ABG55960 | Human bra | 326 | 6 | 3.1 | 65 | 4 | AAM82825 | Human imm |
| 254 | 6 | 3.1 | 52 | 4 | ABG55960 | Human liv | 327 | 6 | 3.1 | 66 | 6 | AAU47962 | Propionib |
| 255 | 6 | 3.1 | 52 | 4 | ABG55960 | Human pep | 328 | 6 | 3.1 | 66 | 6 | ABM44481 | Propionib |
| 256 | 6 | 3.1 | 53 | 4 | ABG41719 | Human pep | 329 | 6 | 3.1 | 67 | 4 | ABG74853 | Human col |
| 257 | 6 | 3.1 | 53 | 4 | ABG41719 | Propionib | 330 | 6 | 3.1 | 70 | 2 | AAU25730 | Human sec |
| 258 | 6 | 3.1 | 53 | 4 | ABG41719 | Propionib | 331 | 6 | 3.1 | 71 | 4 | AAU39618 | Propionib |
| 259 | 6 | 3.1 | 53 | 4 | ABG41719 | Propionib | 332 | 6 | 3.1 | 71 | 4 | AAU39618 | Propionib |
| 260 | 6 | 3.1 | 53 | 4 | ABG41719 | Propionib | 333 | 6 | 3.1 | 71 | 4 | ABM36137 | Propionib |
| 261 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 334 | 6 | 3.1 | 71 | 6 | ABM36137 | Propionib |
| 262 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 335 | 6 | 3.1 | 71 | 6 | ABM36137 | Propionib |
| 263 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 336 | 6 | 3.1 | 72 | 5 | ABP05410 | Human ORF |
| 264 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 337 | 6 | 3.1 | 73 | 4 | AAU53843 | Propionib |
| 265 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 338 | 6 | 3.1 | 73 | 4 | ABM50362 | Propionib |
| 266 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 339 | 6 | 3.1 | 73 | 6 | ABM50362 | Propionib |
| 267 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 340 | 6 | 3.1 | 74 | 3 | ABM58171 | lung can |
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| 278 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 351 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 280 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 353 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 282 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 355 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 283 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 356 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 284 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 357 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 286 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 359 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 292 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 365 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 299 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 372 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 303 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 376 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 304 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 377 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 305 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 378 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 306 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 379 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 308 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 381 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 309 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 382 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 310 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 383 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
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| 315 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 388 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 316 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 389 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |
| 317 | 6 | 3.1 | 54 | 4 | ABM62014 | Propionib | 390 | 6 | 3.1 | 74 | 4 | ABM58171 | lung can |

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|-----|---|-----|----|---|-----------|-----------|-----|---|-----|----|---|----------|-----------|
| 391 | 6 | 3.1 | 78 | 6 | ABR68196 | Human sec | 464 | 6 | 3.1 | 78 | 6 | ABO27313 | Human sec |
| 392 | 6 | 3.1 | 78 | 6 | ABU60588 | Human sec | 465 | 6 | 3.1 | 78 | 6 | ABR68806 | Human sec |
| 393 | 6 | 3.1 | 78 | 6 | ABU96249 | Novel hum | 466 | 6 | 3.1 | 78 | 6 | ABO06622 | Human sec |
| 394 | 6 | 3.1 | 78 | 6 | ABU92680 | Human sec | 467 | 6 | 3.1 | 78 | 6 | ABR99167 | Human sec |
| 395 | 6 | 3.1 | 78 | 6 | ABU02809 | Human sec | 468 | 6 | 3.1 | 78 | 6 | ABU57051 | Human PRO |
| 396 | 6 | 3.1 | 78 | 6 | ABO02809 | Human sec | 469 | 6 | 3.1 | 78 | 6 | ABU86003 | Novel hum |
| 397 | 6 | 3.1 | 78 | 6 | ABR74963 | Human sec | 470 | 6 | 3.1 | 78 | 6 | ABU82290 | Novel hum |
| 398 | 6 | 3.1 | 78 | 6 | ABR94725 | Human sec | 471 | 6 | 3.1 | 78 | 6 | ABU87301 | Human PRO |
| 399 | 6 | 3.1 | 78 | 6 | ABU13970 | Human PRO | 472 | 6 | 3.1 | 78 | 6 | ABU83773 | Human sec |
| 400 | 6 | 3.1 | 78 | 6 | ABU85698 | Human PRO | 473 | 6 | 3.1 | 78 | 6 | ABO08147 | Human PRO |
| 401 | 6 | 3.1 | 78 | 6 | ABU98858 | Novel hum | 474 | 6 | 3.1 | 78 | 6 | ABU92508 | Human sec |
| 402 | 6 | 3.1 | 78 | 6 | ABU98073 | Novel hum | 475 | 6 | 3.1 | 78 | 6 | ABU1858 | Novel hum |
| 403 | 6 | 3.1 | 78 | 6 | ABU91779 | Novel hum | 476 | 6 | 3.1 | 78 | 6 | ABU66022 | Novel hum |
| 404 | 6 | 3.1 | 78 | 6 | ABU89472 | Human PRO | 477 | 6 | 3.1 | 78 | 6 | ABU81178 | Human sec |
| 405 | 6 | 3.1 | 78 | 6 | ABU86313 | Human sec | 478 | 6 | 3.1 | 78 | 6 | ABU59851 | Human sec |
| 406 | 6 | 3.1 | 78 | 6 | ABU67526 | Human sec | 479 | 6 | 3.1 | 78 | 6 | ABU94039 | Novel hum |
| 407 | 6 | 3.1 | 78 | 6 | ABU080554 | Human PRO | 480 | 6 | 3.1 | 78 | 6 | ABU99892 | Novel hum |
| 408 | 6 | 3.1 | 78 | 6 | ABU72555 | Novel hum | 481 | 6 | 3.1 | 78 | 6 | ABR6562 | Human sec |
| 409 | 6 | 3.1 | 78 | 6 | ABU90908 | Novel hum | 482 | 6 | 3.1 | 78 | 6 | ABR90980 | Human sec |
| 410 | 6 | 3.1 | 78 | 6 | ABR99472 | Human sec | 483 | 6 | 3.1 | 78 | 6 | ABO53293 | Novel hum |
| 411 | 6 | 3.1 | 78 | 6 | ABR98862 | Human sec | 484 | 6 | 3.1 | 78 | 6 | ABU59010 | Human sec |
| 412 | 6 | 3.1 | 78 | 6 | ABO16385 | Human sec | 485 | 6 | 3.1 | 78 | 6 | ABU94407 | Human PRO |
| 413 | 6 | 3.1 | 78 | 6 | ABR92285 | Human sec | 486 | 6 | 3.1 | 78 | 6 | ABU79289 | Human PRO |
| 414 | 6 | 3.1 | 78 | 6 | ABO18926 | Human sec | 487 | 6 | 3.1 | 78 | 6 | ABU86618 | Human sec |
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| 421 | 6 | 3.1 | 78 | 6 | ABO02199 | Human sec | 494 | 6 | 3.1 | 78 | 6 | ABR64669 | Human sec |
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| 424 | 6 | 3.1 | 78 | 6 | ABO06269 | Novel hum | 497 | 6 | 3.1 | 78 | 6 | ABU92985 | Human sec |
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| 432 | 6 | 3.1 | 78 | 6 | ABU71538 | Human sec | 505 | 6 | 3.1 | 78 | 6 | ABU87606 | Human PRO |
| 433 | 6 | 3.1 | 78 | 6 | ABU65689 | Human sec | 506 | 6 | 3.1 | 78 | 6 | ABU91474 | Human PRO |
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| 436 | 6 | 3.1 | 78 | 6 | ABR67172 | Human sec | 509 | 6 | 3.1 | 78 | 6 | ABR69778 | Human sec |
| 437 | 6 | 3.1 | 78 | 6 | ABO15775 | Human sec | 510 | 6 | 3.1 | 78 | 6 | ABU80155 | Human PRO |
| 438 | 6 | 3.1 | 78 | 6 | ABU56056 | Human sec | 511 | 6 | 3.1 | 78 | 6 | ABU82507 | Novel hum |
| 439 | 6 | 3.1 | 78 | 6 | ABU72319 | Human PRO | 512 | 6 | 3.1 | 78 | 6 | ABU92219 | Novel hum |
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| 443 | 6 | 3.1 | 78 | 6 | ABO07842 | Human PRO | 516 | 6 | 3.1 | 78 | 6 | ABU96471 | Human PRO |
| 444 | 6 | 3.1 | 78 | 6 | ABR70083 | Human sec | 517 | 6 | 3.1 | 78 | 6 | ABU10925 | Human PRO |
| 445 | 6 | 3.1 | 78 | 6 | ABR69416 | Human sec | 518 | 6 | 3.1 | 78 | 6 | ABU10630 | Human sec |
| 446 | 6 | 3.1 | 78 | 6 | ABO01557 | Human PRO | 519 | 6 | 3.1 | 78 | 6 | ABU81677 | Novel hum |
| 447 | 6 | 3.1 | 78 | 6 | ABU81359 | Human PRO | 520 | 6 | 3.1 | 78 | 6 | ABU72141 | Human PRO |
| 448 | 6 | 3.1 | 78 | 6 | ABR60156 | Human sec | 521 | 6 | 3.1 | 78 | 6 | ABU95639 | Human PRO |
| 449 | 6 | 3.1 | 78 | 6 | ABU90992 | Human PRO | 522 | 6 | 3.1 | 78 | 6 | ABU96848 | Novel hum |
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| 452 | 6 | 3.1 | 78 | 6 | ABR68501 | Human sec | 525 | 6 | 3.1 | 78 | 6 | ABO08452 | Human sec |
| 453 | 6 | 3.1 | 78 | 6 | ABR71913 | Human sec | 526 | 6 | 3.1 | 78 | 6 | ABU88616 | Human PRO |
| 454 | 6 | 3.1 | 78 | 6 | ABU59304 | Human sec | 527 | 6 | 3.1 | 78 | 6 | ABO34130 | Human PRO |
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| 456 | 6 | 3.1 | 78 | 6 | ABU89083 | Human sec | 529 | 6 | 3.1 | 78 | 6 | ABO05659 | Human sec |
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| 459 | 6 | 3.1 | 78 | 6 | ABU90567 | Novel hum | 532 | 6 | 3.1 | 78 | 6 | ABR80937 | Human sec |
| 460 | 6 | 3.1 | 78 | 6 | ABU84078 | Human sec | 533 | 6 | 3.1 | 78 | 6 | ABR81242 | Human sec |
| 461 | 6 | 3.1 | 78 | 6 | ABU93729 | Novel hum | 534 | 6 | 3.1 | 78 | 6 | ABM00938 | Human sec |
| 462 | 6 | 3.1 | 78 | 6 | ABO26001 | Human PRO | 535 | 6 | 3.1 | 78 | 6 | ABR88540 | Human sec |
| 463 | 6 | 3.1 | 78 | 6 | ABR64974 | Human sec | 536 | 6 | 3.1 | 78 | 6 | ABM77361 | Human sec |

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|-----|---|-----|----|---|-----------|-----------|-----|---|-----|----|---|----------|-----------|
| 537 | 6 | 3.1 | 78 | 6 | ABO28845 | Human sec | 610 | 6 | 3.1 | 78 | 6 | ABR87015 | Human sec |
| 538 | 6 | 3.1 | 78 | 6 | ABO31590 | Human sec | 611 | 6 | 3.1 | 78 | 6 | ABM11057 | Human sec |
| 539 | 6 | 3.1 | 78 | 6 | ABM08007 | Human sec | 612 | 6 | 3.1 | 78 | 6 | ABM28201 | Human sec |
| 540 | 6 | 3.1 | 78 | 6 | ABO40487 | Human sec | 613 | 6 | 3.1 | 78 | 6 | ABO32200 | Human sec |
| 541 | 6 | 3.1 | 78 | 6 | ABO35912 | Human PRO | 614 | 6 | 3.1 | 78 | 6 | ABM15327 | Human sec |
| 542 | 6 | 3.1 | 78 | 6 | ABO44051 | Human PRO | 615 | 6 | 3.1 | 78 | 6 | ABM06482 | Human sec |
| 543 | 6 | 3.1 | 78 | 6 | ADA77994 | Human sec | 616 | 6 | 3.1 | 78 | 6 | ABM06482 | Human sec |
| 544 | 6 | 3.1 | 78 | 6 | ABM24846 | Human sec | 617 | 6 | 3.1 | 78 | 6 | ABM04293 | Human sec |
| 545 | 6 | 3.1 | 78 | 6 | ABO03114 | Human sec | 618 | 6 | 3.1 | 78 | 6 | ABM22406 | Human sec |
| 546 | 6 | 3.1 | 78 | 6 | ABR903170 | Human sec | 619 | 6 | 3.1 | 78 | 6 | ABM07702 | Human sec |
| 547 | 6 | 3.1 | 78 | 6 | ABM17284 | Human sec | 620 | 6 | 3.1 | 78 | 6 | ABO40792 | Human sec |
| 548 | 6 | 3.1 | 78 | 6 | ABR95030 | Human sec | 621 | 6 | 3.1 | 78 | 6 | ABM35439 | Human sec |
| 549 | 6 | 3.1 | 78 | 6 | ABR95335 | Human sec | 622 | 6 | 3.1 | 78 | 6 | ABM33202 | Human sec |
| 550 | 6 | 3.1 | 78 | 6 | ABM17123 | Human tra | 623 | 6 | 3.1 | 78 | 6 | ABO52728 | Human PRO |
| 551 | 6 | 3.1 | 78 | 6 | ABO21573 | Human sec | 624 | 6 | 3.1 | 78 | 6 | ABO50288 | Human sec |
| 552 | 6 | 3.1 | 78 | 6 | ABR97837 | Human sec | 625 | 6 | 3.1 | 78 | 6 | ABU99282 | Human sec |
| 553 | 6 | 3.1 | 78 | 6 | ABR87625 | Human sec | 626 | 6 | 3.1 | 78 | 6 | ABO04334 | Human sec |
| 554 | 6 | 3.1 | 78 | 6 | ABM77666 | Human sec | 627 | 6 | 3.1 | 78 | 6 | ABO05964 | Human sec |
| 555 | 6 | 3.1 | 78 | 6 | ABM27896 | Human sec | 628 | 6 | 3.1 | 78 | 6 | ABM18504 | Human sec |
| 556 | 6 | 3.1 | 78 | 6 | ABM06177 | Human sec | 629 | 6 | 3.1 | 78 | 6 | ADA27999 | Human sec |
| 557 | 6 | 3.1 | 78 | 6 | ABM03683 | Human sec | 630 | 6 | 3.1 | 78 | 6 | ABR97532 | Human sec |
| 558 | 6 | 3.1 | 78 | 6 | ABM35134 | Human sec | 631 | 6 | 3.1 | 78 | 6 | ABR80632 | Human sec |
| 559 | 6 | 3.1 | 78 | 6 | ABM26371 | Human sec | 632 | 6 | 3.1 | 78 | 6 | ABM01243 | Human sec |
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| 561 | 6 | 3.1 | 78 | 6 | ABR92895 | Human sec | 634 | 6 | 3.1 | 78 | 6 | ABM13497 | Human sec |
| 562 | 6 | 3.1 | 78 | 6 | ABO24656 | Human sec | 635 | 6 | 3.1 | 78 | 6 | ABM20881 | Human sec |
| 563 | 6 | 3.1 | 78 | 6 | ADA37874 | Human sec | 636 | 6 | 3.1 | 78 | 6 | ABO42012 | Human sec |
| 564 | 6 | 3.1 | 78 | 6 | ABM11667 | Human sec | 637 | 6 | 3.1 | 78 | 6 | ABO42622 | Human sec |
| 565 | 6 | 3.1 | 78 | 6 | ABM02768 | Human sec | 638 | 6 | 3.1 | 78 | 6 | ABM10142 | Human sec |
| 566 | 6 | 3.1 | 78 | 6 | ABM16064 | Human sec | 639 | 6 | 3.1 | 78 | 6 | ABO38657 | Human sec |
| 567 | 6 | 3.1 | 78 | 6 | ABO27625 | Human sec | 640 | 6 | 3.1 | 78 | 6 | ABM32897 | Human sec |
| 568 | 6 | 3.1 | 78 | 6 | ABM29116 | Human sec | 641 | 6 | 3.1 | 78 | 6 | ABM22711 | Human sec |
| 569 | 6 | 3.1 | 78 | 6 | ABM07092 | Human sec | 642 | 6 | 3.1 | 78 | 6 | ABM74922 | Human sec |
| 570 | 6 | 3.1 | 78 | 6 | ABM21186 | Human sec | 643 | 6 | 3.1 | 78 | 6 | ADA79786 | Human sec |
| 571 | 6 | 3.1 | 78 | 6 | ABM09532 | Human sec | 644 | 6 | 3.1 | 78 | 6 | ABR96312 | Human sec |
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| 573 | 6 | 3.1 | 78 | 6 | ABO36217 | Human PRO | 646 | 6 | 3.1 | 78 | 6 | ABR86710 | Human sec |
| 574 | 6 | 3.1 | 78 | 6 | ABO43746 | Human PRO | 647 | 6 | 3.1 | 78 | 6 | ABM16674 | Human sec |
| 575 | 6 | 3.1 | 78 | 6 | ABM76446 | Human sec | 648 | 6 | 3.1 | 78 | 6 | ABM29726 | Human sec |
| 576 | 6 | 3.1 | 78 | 6 | ABM76142 | Human sec | 649 | 6 | 3.1 | 78 | 6 | ABO29150 | Human sec |
| 577 | 6 | 3.1 | 78 | 6 | ABM25761 | Human sec | 650 | 6 | 3.1 | 78 | 6 | ABM23321 | Human sec |
| 578 | 6 | 3.1 | 78 | 6 | ABM26066 | Human sec | 651 | 6 | 3.1 | 78 | 6 | ABM22101 | Human sec |
| 579 | 6 | 3.1 | 78 | 6 | ADA21560 | Human sec | 652 | 6 | 3.1 | 78 | 6 | ABO37742 | Human sec |
| 580 | 6 | 3.1 | 78 | 6 | ABO03419 | Human sec | 653 | 6 | 3.1 | 78 | 6 | ABM28506 | Human sec |
| 581 | 6 | 3.1 | 78 | 6 | ABO02504 | Human sec | 654 | 6 | 3.1 | 78 | 6 | ABM28811 | Human sec |
| 582 | 6 | 3.1 | 78 | 6 | ABO44271 | Human sec | 655 | 6 | 3.1 | 78 | 6 | ABM66455 | Human sec |
| 583 | 6 | 3.1 | 78 | 6 | ABR90675 | Human sec | 656 | 6 | 3.1 | 78 | 6 | ABM75837 | Human sec |
| 584 | 6 | 3.1 | 78 | 6 | ABR73743 | Human sec | 657 | 6 | 3.1 | 78 | 6 | ABM34117 | Human sec |
| 585 | 6 | 3.1 | 78 | 6 | ABO16995 | Human sec | 658 | 6 | 3.1 | 78 | 6 | ABM34422 | Human sec |
| 586 | 6 | 3.1 | 78 | 6 | ABR94420 | Human sec | 659 | 6 | 3.1 | 78 | 6 | ABO20353 | Human sec |
| 587 | 6 | 3.1 | 78 | 6 | ABR75927 | Human sec | 660 | 6 | 3.1 | 78 | 6 | ABO21268 | Human sec |
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| 589 | 6 | 3.1 | 78 | 6 | ABR93200 | Human sec | 662 | 6 | 3.1 | 78 | 6 | ADA20100 | Novel hum |
| 590 | 6 | 3.1 | 78 | 6 | ABR93505 | Human sec | 663 | 6 | 3.1 | 78 | 6 | ABO34199 | Human sec |
| 591 | 6 | 3.1 | 78 | 6 | ADA10347 | Human sec | 664 | 6 | 3.1 | 78 | 6 | ABO34117 | Human sec |
| 592 | 6 | 3.1 | 78 | 6 | ABR87930 | Human sec | 665 | 6 | 3.1 | 78 | 6 | ABR96617 | Human sec |
| 593 | 6 | 3.1 | 78 | 6 | ABO30065 | Human sec | 666 | 6 | 3.1 | 78 | 6 | ADA94579 | Human sec |
| 594 | 6 | 3.1 | 78 | 6 | ABO33274 | Human sec | 667 | 6 | 3.1 | 78 | 6 | ABR85795 | Human sec |
| 595 | 6 | 3.1 | 78 | 6 | ABM04962 | Human sec | 668 | 6 | 3.1 | 78 | 6 | ABR99777 | Human sec |
| 596 | 6 | 3.1 | 78 | 6 | ABO33274 | Human sec | 669 | 6 | 3.1 | 78 | 6 | ABM00328 | Human sec |
| 597 | 6 | 3.1 | 78 | 6 | ABM08922 | Human sec | 670 | 6 | 3.1 | 78 | 6 | ABM00633 | Human sec |
| 598 | 6 | 3.1 | 78 | 6 | ABO36522 | Human sec | 671 | 6 | 3.1 | 78 | 6 | ABO29760 | Human sec |
| 599 | 6 | 3.1 | 78 | 6 | ABO35607 | Human sec | 672 | 6 | 3.1 | 78 | 6 | ABM23626 | Human sec |
| 600 | 6 | 3.1 | 78 | 6 | ABO39572 | Human sec | 673 | 6 | 3.1 | 78 | 6 | ABM29421 | Human sec |
| 601 | 6 | 3.1 | 78 | 6 | ABM10447 | Human sec | 674 | 6 | 3.1 | 78 | 6 | ABO38352 | Human sec |
| 602 | 6 | 3.1 | 78 | 6 | ABM11972 | Human sec | 675 | 6 | 3.1 | 78 | 6 | ABO45652 | Human sec |
| 603 | 6 | 3.1 | 78 | 6 | ABO52118 | Human PRO | 676 | 6 | 3.1 | 78 | 6 | ABO45652 | Human PRO |
| 604 | 6 | 3.1 | 78 | 6 | ABO52423 | Human PRO | 677 | 6 | 3.1 | 78 | 6 | ABO16690 | Human sec |
| 605 | 6 | 3.1 | 78 | 6 | ADA19928 | Novel hum | 678 | 6 | 3.1 | 78 | 6 | ABO18316 | Human sec |
| 606 | 6 | 3.1 | 78 | 6 | ABO23741 | Human sec | 679 | 6 | 3.1 | 78 | 6 | ABO22743 | Human PRO |
| 607 | 6 | 3.1 | 78 | 6 | ADBI17311 | Human tra | 680 | 6 | 3.1 | 78 | 6 | ABO23048 | Human PRO |
| 608 | 6 | 3.1 | 78 | 6 | ADAI17891 | Human PRO | 681 | 6 | 3.1 | 78 | 6 | ABR92590 | Human sec |
| 609 | 6 | 3.1 | 78 | 6 | ABR97227 | Human sec | 682 | 6 | 3.1 | 78 | 6 | | |

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|-----|---|-----|----|---|----------|-----|---|-----|----|---|----------|-----|---|----------|-----------|
| 683 | 6 | 3.1 | 78 | 6 | ABR81547 | 756 | 6 | 3.1 | 78 | 6 | ADA00397 | 110 | 6 | ADA00397 | Human sec |
| 684 | 6 | 3.1 | 78 | 6 | ABR77971 | 757 | 6 | 3.1 | 78 | 6 | ABM26981 | 111 | 6 | ABM26981 | Human sec |
| 685 | 6 | 3.1 | 78 | 6 | ABR89760 | 758 | 6 | 3.1 | 78 | 6 | ABO03378 | 112 | 6 | ABO03378 | Human sec |
| 686 | 6 | 3.1 | 78 | 6 | ABM26676 | 759 | 6 | 3.1 | 78 | 6 | ABO39877 | 113 | 6 | ABO39877 | Human sec |
| 687 | 6 | 3.1 | 78 | 6 | ABM13802 | 760 | 6 | 3.1 | 78 | 7 | ABO49983 | 114 | 6 | ABO49983 | Human sec |
| 688 | 6 | 3.1 | 78 | 6 | ABO28540 | 761 | 6 | 3.1 | 78 | 7 | ABO50898 | 115 | 6 | ABO50898 | Human sec |
| 689 | 6 | 3.1 | 78 | 6 | ABO30370 | 762 | 6 | 3.1 | 78 | 7 | ABO05354 | 116 | 6 | ABO05354 | Human sec |
| 690 | 6 | 3.1 | 78 | 6 | ABM07397 | 763 | 6 | 3.1 | 78 | 7 | ABR74658 | 117 | 6 | ABR74658 | Human sec |
| 691 | 6 | 3.1 | 78 | 6 | ABM03988 | 764 | 6 | 3.1 | 78 | 7 | ABR77137 | 118 | 6 | ABR77137 | Human sec |
| 692 | 6 | 3.1 | 78 | 6 | ABO37132 | 765 | 6 | 3.1 | 78 | 7 | ABM17894 | 119 | 6 | ABM17894 | Human sec |
| 693 | 6 | 3.1 | 78 | 6 | ABO41707 | 766 | 6 | 3.1 | 78 | 7 | ABR95945 | 120 | 6 | ABR95945 | Human sec |
| 694 | 6 | 3.1 | 78 | 6 | ABO35302 | 767 | 6 | 3.1 | 78 | 7 | ABO21878 | 121 | 6 | ABO21878 | Human sec |
| 695 | 6 | 3.1 | 78 | 6 | ABM25151 | 768 | 6 | 3.1 | 78 | 7 | ABO20048 | 122 | 6 | ABO20048 | Human sec |
| 696 | 6 | 3.1 | 78 | 6 | ABO47543 | 769 | 6 | 3.1 | 78 | 7 | ABO24351 | 123 | 6 | ABO24351 | Human sec |
| 697 | 6 | 3.1 | 78 | 6 | ABO47848 | 770 | 6 | 3.1 | 78 | 7 | ABR86100 | 124 | 6 | ABR86100 | Human sec |
| 698 | 6 | 3.1 | 78 | 6 | ABO48458 | 771 | 6 | 3.1 | 78 | 7 | ABM10752 | 125 | 6 | ABM10752 | Human sec |
| 699 | 6 | 3.1 | 78 | 6 | ABO51508 | 772 | 6 | 3.1 | 78 | 7 | ABM76751 | 126 | 6 | ABM76751 | Human sec |
| 700 | 6 | 3.1 | 78 | 6 | ABO51813 | 773 | 6 | 3.1 | 78 | 7 | ABR89455 | 127 | 6 | ABR89455 | Human sec |
| 701 | 6 | 3.1 | 78 | 6 | ABO50593 | 774 | 6 | 3.1 | 78 | 7 | ABM12582 | 128 | 6 | ABM12582 | Human sec |
| 702 | 6 | 3.1 | 78 | 6 | ABR79717 | 775 | 6 | 3.1 | 78 | 7 | ABO05872 | 129 | 6 | ABO05872 | Human sec |
| 703 | 6 | 3.1 | 78 | 6 | ABM16979 | 776 | 6 | 3.1 | 78 | 7 | ABO34997 | 130 | 6 | ABO34997 | Human PRO |
| 704 | 6 | 3.1 | 78 | 6 | ABO18011 | 777 | 6 | 3.1 | 78 | 7 | ABM03073 | 131 | 6 | ABM03073 | Human sec |
| 705 | 6 | 3.1 | 78 | 6 | ABR96922 | 778 | 6 | 3.1 | 78 | 7 | ABM19051 | 132 | 6 | ABM19051 | Human sec |
| 706 | 6 | 3.1 | 78 | 6 | ADA38804 | 779 | 6 | 3.1 | 78 | 7 | ABM19356 | 133 | 6 | ABM19356 | Human sec |
| 707 | 6 | 3.1 | 78 | 6 | ABM12277 | 780 | 6 | 3.1 | 78 | 7 | ABO46567 | 134 | 6 | ABO46567 | Human PRO |
| 708 | 6 | 3.1 | 78 | 6 | ABM16369 | 781 | 6 | 3.1 | 78 | 7 | ABO49068 | 135 | 6 | ABO49068 | Human sec |
| 709 | 6 | 3.1 | 78 | 6 | ABM24236 | 782 | 6 | 3.1 | 78 | 7 | ABR69111 | 136 | 6 | ABR69111 | Human sec |
| 710 | 6 | 3.1 | 78 | 6 | ABM14717 | 783 | 6 | 3.1 | 78 | 7 | ABR89150 | 137 | 6 | ABR89150 | Human sec |
| 711 | 6 | 3.1 | 78 | 6 | ABM04598 | 784 | 6 | 3.1 | 78 | 7 | ABR72523 | 138 | 6 | ABR72523 | Human sec |
| 712 | 6 | 3.1 | 78 | 6 | ABM09227 | 785 | 6 | 3.1 | 78 | 7 | ABR74353 | 139 | 6 | ABR74353 | Human sec |
| 713 | 6 | 3.1 | 78 | 6 | ABM06787 | 786 | 6 | 3.1 | 78 | 7 | ABO18621 | 140 | 6 | ABO18621 | Human sec |
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| 715 | 6 | 3.1 | 78 | 6 | ABM75532 | 788 | 6 | 3.1 | 78 | 7 | ABM01548 | 142 | 6 | ABM01548 | Human sec |
| 716 | 6 | 3.1 | 78 | 6 | ABM25456 | 789 | 6 | 3.1 | 78 | 7 | ABM02158 | 143 | 6 | ABM02158 | Human sec |
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| 718 | 6 | 3.1 | 78 | 6 | ABO46872 | 791 | 6 | 3.1 | 78 | 7 | ABM12887 | 145 | 6 | ABM12887 | Human sec |
| 719 | 6 | 3.1 | 78 | 6 | ABO47177 | 792 | 6 | 3.1 | 78 | 7 | ABM30641 | 146 | 6 | ABM30641 | Human sec |
| 720 | 6 | 3.1 | 78 | 6 | ABO47177 | 793 | 6 | 3.1 | 78 | 7 | ABM24541 | 147 | 6 | ABM24541 | Human sec |
| 721 | 6 | 3.1 | 78 | 6 | ADA83311 | 794 | 6 | 3.1 | 78 | 7 | ABO29455 | 148 | 6 | ABO29455 | Human sec |
| 722 | 6 | 3.1 | 78 | 6 | ABR71608 | 795 | 6 | 3.1 | 78 | 7 | ABO31285 | 149 | 6 | ABO31285 | Human sec |
| 723 | 6 | 3.1 | 78 | 6 | ABR72218 | 796 | 6 | 3.1 | 78 | 7 | ABM14412 | 150 | 6 | ABM14412 | Human sec |
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| 725 | 6 | 3.1 | 78 | 6 | ABO06927 | 798 | 6 | 3.1 | 78 | 7 | ABO38962 | 152 | 6 | ABO38962 | Human sec |
| 726 | 6 | 3.1 | 78 | 6 | ABR84880 | 799 | 6 | 3.1 | 78 | 7 | ABM34727 | 153 | 6 | ABM34727 | Human sec |
| 727 | 6 | 3.1 | 78 | 6 | ABR73438 | 800 | 6 | 3.1 | 78 | 7 | ABO51203 | 154 | 6 | ABO51203 | Human sec |
| 728 | 6 | 3.1 | 78 | 6 | ABR76532 | 801 | 6 | 3.1 | 78 | 7 | ABO04029 | 155 | 6 | ABO04029 | Human sec |
| 729 | 6 | 3.1 | 78 | 6 | ABR73333 | 802 | 6 | 3.1 | 78 | 7 | ABO10499 | 156 | 6 | ABO10499 | Human PRO |
| 730 | 6 | 3.1 | 78 | 6 | ABM18199 | 803 | 6 | 3.1 | 78 | 7 | ABO53216 | 157 | 6 | ABO53216 | Human sec |
| 731 | 6 | 3.1 | 78 | 6 | ABO20658 | 804 | 6 | 3.1 | 78 | 7 | ABR77742 | 158 | 6 | ABR77742 | Human sec |
| 732 | 6 | 3.1 | 78 | 6 | ABO25401 | 805 | 6 | 3.1 | 78 | 7 | ABR78952 | 159 | 6 | ABR78952 | Human sec |
| 733 | 6 | 3.1 | 78 | 6 | ABO25706 | 806 | 6 | 3.1 | 78 | 7 | ABO24046 | 160 | 6 | ABO24046 | Human sec |
| 734 | 6 | 3.1 | 78 | 6 | ABR94115 | 807 | 6 | 3.1 | 78 | 7 | ABR93810 | 161 | 6 | ABR93810 | Human sec |
| 735 | 6 | 3.1 | 78 | 6 | ADA92325 | 808 | 6 | 3.1 | 78 | 7 | ABM01853 | 162 | 6 | ABM01853 | Human sec |
| 736 | 6 | 3.1 | 78 | 6 | ABR80022 | 809 | 6 | 3.1 | 78 | 7 | ABM78276 | 163 | 6 | ABM78276 | Human sec |
| 737 | 6 | 3.1 | 78 | 6 | ABM11362 | 810 | 6 | 3.1 | 78 | 7 | ABR90065 | 164 | 6 | ABR90065 | Human sec |
| 738 | 6 | 3.1 | 78 | 6 | ABO32969 | 811 | 6 | 3.1 | 78 | 7 | ADA22486 | 165 | 6 | ADA22486 | Human sec |
| 739 | 6 | 3.1 | 78 | 6 | ABO30675 | 812 | 6 | 3.1 | 78 | 7 | ABM27591 | 166 | 6 | ABM27591 | Human sec |
| 740 | 6 | 3.1 | 78 | 6 | ABO30980 | 813 | 6 | 3.1 | 78 | 7 | ABM13192 | 167 | 6 | ABM13192 | Human sec |
| 741 | 6 | 3.1 | 78 | 6 | ABM27286 | 814 | 6 | 3.1 | 78 | 7 | ABM14107 | 168 | 6 | ABM14107 | Human sec |
| 742 | 6 | 3.1 | 78 | 6 | ABM05567 | 815 | 6 | 3.1 | 78 | 7 | ABM08312 | 169 | 6 | ABM08312 | Human sec |
| 743 | 6 | 3.1 | 78 | 6 | ABM15632 | 816 | 6 | 3.1 | 78 | 7 | ABO40182 | 170 | 6 | ABO40182 | Human sec |
| 744 | 6 | 3.1 | 78 | 6 | ABM08617 | 817 | 6 | 3.1 | 78 | 7 | ABM74617 | 171 | 6 | ABM74617 | Human sec |
| 745 | 6 | 3.1 | 78 | 6 | ABM08617 | 818 | 6 | 3.1 | 78 | 7 | ABM33812 | 172 | 6 | ABM33812 | Human sec |
| 746 | 6 | 3.1 | 78 | 6 | ABO42317 | 819 | 6 | 3.1 | 78 | 7 | ABM20271 | 173 | 6 | ABM20271 | Human sec |
| 747 | 6 | 3.1 | 78 | 6 | ABO38047 | 820 | 6 | 3.1 | 78 | 7 | ABO48763 | 174 | 6 | ABO48763 | Human sec |
| 748 | 6 | 3.1 | 78 | 6 | ABO45957 | 821 | 6 | 3.1 | 78 | 7 | ABO22586 | 175 | 6 | ABO22586 | Human sec |
| 749 | 6 | 3.1 | 78 | 6 | ABM66760 | 822 | 6 | 3.1 | 78 | 7 | ABR72828 | 176 | 6 | ABR72828 | Human sec |
| 750 | 6 | 3.1 | 78 | 6 | ADB20354 | 823 | 6 | 3.1 | 78 | 7 | ABO15470 | 177 | 6 | ABO15470 | Human sec |
| 751 | 6 | 3.1 | 78 | 6 | ABM19661 | 824 | 6 | 3.1 | 78 | 7 | ABR85185 | 178 | 6 | ABR85185 | Human sec |
| 752 | 6 | 3.1 | 78 | 6 | ABO49373 | 825 | 6 | 3.1 | 78 | 7 | ABO15165 | 179 | 6 | ABO15165 | Human sec |
| 753 | 6 | 3.1 | 78 | 6 | ABO49678 | 826 | 6 | 3.1 | 78 | 7 | ABO17300 | 180 | 6 | ABO17300 | Human sec |
| 754 | 6 | 3.1 | 78 | 6 | ADA78606 | 827 | 6 | 3.1 | 78 | 7 | ABM17589 | 181 | 6 | ABM17589 | Human sec |
| 755 | 6 | 3.1 | 78 | 6 | ABR88235 | 828 | 6 | 3.1 | 78 | 7 | ABM17589 | 182 | 6 | ABM17589 | Human sec |

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|-----|---|-----|----|---|-----------|-----------|-----|---|-----|----|---|----------|-----------|
| 829 | 6 | 3.1 | 78 | 7 | ADA06652 | Human sec | 902 | 6 | 3.1 | 83 | 4 | ABG28185 | Novel hum |
| 830 | 6 | 3.1 | 78 | 7 | ADA39345 | Human sec | 903 | 6 | 3.1 | 84 | 5 | ABP27263 | Streptoco |
| 831 | 6 | 3.1 | 78 | 7 | ABR85490 | Human sec | 904 | 6 | 3.1 | 85 | 2 | AAW69237 | Mouse dec |
| 832 | 6 | 3.1 | 78 | 7 | ABM77056 | Human sec | 905 | 6 | 3.1 | 85 | 2 | AAW19618 | Peptide # |
| 833 | 6 | 3.1 | 78 | 7 | ABO28235 | Human sec | 906 | 6 | 3.1 | 85 | 4 | ABB39272 | Peptide # |
| 834 | 6 | 3.1 | 78 | 7 | ABM23016 | Human sec | 907 | 6 | 3.1 | 85 | 4 | AAW32775 | Peptide # |
| 835 | 6 | 3.1 | 78 | 7 | ABM30336 | Human sec | 908 | 6 | 3.1 | 85 | 4 | AAW24101 | Protein # |
| 836 | 6 | 3.1 | 78 | 7 | ABM21796 | Human sec | 909 | 6 | 3.1 | 85 | 4 | AAW2531 | Human bon |
| 837 | 6 | 3.1 | 78 | 7 | ABM21491 | Human sec | 910 | 6 | 3.1 | 85 | 4 | AAW72531 | Human bon |
| 838 | 6 | 3.1 | 78 | 7 | ABM15022 | Human sec | 911 | 6 | 3.1 | 85 | 4 | AAW13783 | Human pol |
| 839 | 6 | 3.1 | 78 | 7 | ABO41097 | Human sec | 912 | 6 | 3.1 | 85 | 4 | AAW59936 | Human bra |
| 840 | 6 | 3.1 | 78 | 7 | ABO36827 | Human sec | 913 | 6 | 3.1 | 85 | 4 | ABG54222 | Human liv |
| 841 | 6 | 3.1 | 78 | 7 | ABO37437 | Human sec | 914 | 6 | 3.1 | 86 | 5 | ABG42351 | Human pep |
| 842 | 6 | 3.1 | 78 | 7 | ABM75227 | Human sec | 915 | 6 | 3.1 | 86 | 4 | ABG01370 | Human gen |
| 843 | 6 | 3.1 | 78 | 7 | ABM33507 | Human sec | 916 | 6 | 3.1 | 86 | 4 | ABB38901 | Peptide # |
| 844 | 6 | 3.1 | 78 | 7 | ABO46262 | Human sec | 917 | 6 | 3.1 | 86 | 4 | AAW32383 | Peptide # |
| 845 | 6 | 3.1 | 78 | 7 | ADAB2677 | Human sec | 918 | 6 | 3.1 | 86 | 4 | AAW23894 | Protein # |
| 846 | 6 | 3.1 | 78 | 7 | ADAB85639 | Human PRO | 919 | 6 | 3.1 | 86 | 4 | AAW72121 | Human bon |
| 847 | 6 | 3.1 | 78 | 7 | ABM96371 | Human PRO | 920 | 6 | 3.1 | 86 | 4 | AAW59552 | Human bra |
| 848 | 6 | 3.1 | 78 | 7 | ABM31861 | Human sec | 921 | 6 | 3.1 | 86 | 4 | ABG53807 | Human liv |
| 849 | 6 | 3.1 | 78 | 7 | ABM31251 | Human sec | 922 | 6 | 3.1 | 86 | 5 | ABG41935 | Human pep |
| 850 | 6 | 3.1 | 78 | 7 | ABM85985 | Human sec | 923 | 6 | 3.1 | 86 | 5 | ABG64121 | Human alb |
| 851 | 6 | 3.1 | 78 | 7 | ABM32166 | Human sec | 924 | 6 | 3.1 | 86 | 5 | ABP34623 | Human ORF |
| 852 | 6 | 3.1 | 78 | 7 | ABM32471 | Human sec | 925 | 6 | 3.1 | 87 | 4 | ABP41455 | Peptide # |
| 853 | 6 | 3.1 | 78 | 7 | ADB68318 | Human PRO | 926 | 6 | 3.1 | 87 | 4 | ABB39647 | Peptide # |
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| 855 | 6 | 3.1 | 78 | 7 | ABM31556 | Human sec | 928 | 6 | 3.1 | 87 | 4 | ABB24327 | Protein # |
| 856 | 6 | 3.1 | 78 | 7 | ABM30946 | Human sec | 929 | 6 | 3.1 | 87 | 4 | AAW75130 | Human bon |
| 857 | 6 | 3.1 | 78 | 7 | ADB90942 | Novel hum | 930 | 6 | 3.1 | 87 | 4 | AAW72995 | Human bon |
| 858 | 6 | 3.1 | 78 | 7 | ADCS57843 | Human PRO | 931 | 6 | 3.1 | 87 | 4 | AAW60359 | Human bra |
| 859 | 6 | 3.1 | 78 | 7 | ADCS5207 | Human PRO | 932 | 6 | 3.1 | 87 | 4 | AAW62329 | Human bra |
| 860 | 6 | 3.1 | 78 | 7 | ADC12074 | Human sec | 933 | 6 | 3.1 | 87 | 4 | ABG54706 | Human liv |
| 861 | 6 | 3.1 | 78 | 7 | ADC07022 | Human PRO | 934 | 6 | 3.1 | 87 | 5 | ABG56893 | Human liv |
| 862 | 6 | 3.1 | 78 | 7 | ADCS6496 | Human PRO | 935 | 6 | 3.1 | 87 | 5 | ABG44807 | Human pep |
| 863 | 6 | 3.1 | 78 | 7 | ADCL17201 | Mammalian | 936 | 6 | 3.1 | 89 | 4 | AAW73176 | Human bon |
| 864 | 6 | 3.1 | 78 | 7 | ADC07551 | Human sec | 937 | 6 | 3.1 | 89 | 4 | AAW60521 | Human bra |
| 865 | 6 | 3.1 | 78 | 7 | ADCL11541 | Human sec | 938 | 6 | 3.1 | 89 | 4 | ABG54893 | Human liv |
| 866 | 6 | 3.1 | 78 | 7 | ADCL14899 | Novel hum | 939 | 6 | 3.1 | 89 | 4 | AAU20122 | Human DNA |
| 867 | 6 | 3.1 | 78 | 7 | ADCS2394 | Novel hum | 940 | 6 | 3.1 | 89 | 5 | ABG43023 | Human pep |
| 868 | 6 | 3.1 | 78 | 7 | ADCL14663 | Novel hum | 941 | 6 | 3.1 | 89 | 5 | ABG91371 | Novel hum |
| 869 | 6 | 3.1 | 78 | 7 | ADDO08195 | Novel hum | 942 | 6 | 3.1 | 90 | 4 | AAU41384 | Human pol |
| 870 | 6 | 3.1 | 78 | 7 | ADCS2020 | Human PRO | 943 | 6 | 3.1 | 90 | 4 | AAU41384 | Human pol |
| 871 | 6 | 3.1 | 78 | 7 | ADDO7662 | Novel hum | 944 | 6 | 3.1 | 90 | 4 | AAU41384 | Human pol |
| 872 | 6 | 3.1 | 78 | 7 | ADCS2553 | Human PRO | 945 | 6 | 3.1 | 91 | 2 | AAU27150 | Protein e |
| 873 | 6 | 3.1 | 78 | 7 | ADDO5715 | Human sec | 946 | 6 | 3.1 | 91 | 2 | AAU27150 | Protein e |
| 874 | 6 | 3.1 | 78 | 7 | ADDO08733 | Novel hum | 947 | 6 | 3.1 | 91 | 3 | AAU27150 | Protein e |
| 875 | 6 | 3.1 | 78 | 7 | ADDO06982 | Novel hum | 948 | 6 | 3.1 | 91 | 3 | AAU27150 | Protein e |
| 876 | 6 | 3.1 | 78 | 7 | ADCS3229 | Human PRO | 949 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 877 | 6 | 3.1 | 78 | 7 | ADP55336 | Human PRO | 950 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 878 | 6 | 3.1 | 78 | 7 | ADP36070 | Novel hum | 951 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 879 | 6 | 3.1 | 78 | 7 | ADP56294 | Human PRO | 952 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 880 | 6 | 3.1 | 78 | 7 | ADP54732 | Human PRO | 953 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 881 | 6 | 3.1 | 78 | 7 | ADP56886 | Novel hum | 954 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 882 | 6 | 3.1 | 78 | 7 | ADP562353 | Novel hum | 955 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 883 | 6 | 3.1 | 78 | 7 | ADCS2204 | Novel hum | 956 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 884 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 957 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 885 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 958 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 886 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 959 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 887 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 960 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 888 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 961 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 889 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 962 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 890 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 963 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 891 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 964 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 892 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 965 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 893 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 966 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 894 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 967 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 895 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 968 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 896 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 969 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 897 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 970 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 898 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 971 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 899 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 972 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 900 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 973 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |
| 901 | 6 | 3.1 | 78 | 7 | ADP74379 | Human sec | 974 | 6 | 3.1 | 91 | 4 | AAU27150 | Protein e |

975 6 3.1 98 5 ABP10105
976 6 3.1 98 5 ABG44514
977 6 3.1 99 4 AAM18386
978 6 3.1 99 4 AAM17289
979 6 3.1 99 4 ABB36294
980 6 3.1 99 4 ABB37417
981 6 3.1 99 4 AAM29789
982 6 3.1 99 4 AAM30865
983 6 3.1 99 4 ABB31098
984 6 3.1 99 4 ABB32171
985 6 3.1 99 4 ABB27115
986 6 3.1 99 4 AAM70545
987 6 3.1 99 4 AAM57065
988 6 3.1 99 4 AAM58098
989 6 3.1 99 4 AAG51129
990 6 3.1 99 4 AAG52224
991 6 3.1 99 4 AAM05983
992 6 3.1 99 5 ABG39076
993 6 3.1 99 5 ABG40200
994 6 3.1 100 4 ABB11267
995 6 3.1 101 4 ABB11285
996 6 3.1 102 7 ADD12477
997 6 3.1 103 4 AAU41738
998 6 3.1 103 5 ABP03545
999 6 3.1 103 6 ABM38257
1000 6 3.1 106 5 AAE20908

ALIGNMENTS

RESULT 1
ADA57403
ID ADA57403 standard; protein; 194 AA.

XX AC ADA57403;
XX AC
XX DT 20-NOV-2003 (first entry)
XX DT
XX DE Human secreted protein #204.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytosolic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.
XX WO2002102994-A2.
XX 27-DEC-2002.
XX PD

XX 19-MAR-2002; 2002WO-US008278.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;
XX PI
XX WPI; 2003-167512/16.
XX N-PSDB; ADA56510.
XX

XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or

PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1596; 1754pp; English.

PS The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders, or polypeptides comprising an amino acid
XX sequence at least 95% identical to the new sequences. The polypeptides,
XX antibodies or antibody fragments that bind to the polypeptides, nucleic
XX acids encoding the polypeptides, agonists or antagonists that binds to
XX the polypeptide, are useful in preparing diagnostic or pharmaceutical
XX compositions for diagnosing, treating or preventing an e.g. immune
XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,
XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX polynucleotides are useful for chromosome identification, chromosome
XX mapping, for controlling gene expression through triple helix formation
XX or antisense DNA or RNA, in gene therapy, for identifying individuals
XX from minute biological samples, in forensic biology, and as hybridization
XX probes. The polypeptides are useful for as molecular weight markers on
XX sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
XX gels, to raise antibodies, for testing biological activities, and for
XX treating or preventing neural disorders, immune system disorders,
XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX renal, proliferative and/or cancerous diseases. This sequence corresponds
XX to one of the polypeptide of the invention. Note: The sequence data for
XX this patent did form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 194 AA;

Query Match 99.5%; Score 193; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.7e-186;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGLVWLISGGGLAOSDTSPTDEESVSDMGLRHLSGFSVNSYFDSFLELGGK 60
Db 1 MKLASGLVWLISGGGLAOSDTSPTDEESVSDMGLRHLSGFSVNSYFDSFLELGGK 60
QY 61 NGVCQYRCRYGKAPMPRPYKQFPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
Db 61 NGVCQYRCRYGKAPMPRPYKQFPNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
QY 121 TCGANKYRCDAKFRWCLXSLCSDLKRSIGFVSKVEACDSLVDTVTNTWTLCGRPFMNSQ 180
Db 121 TCGANKYRCDAKFRWCLXSLCSDLKRSIGFVSKVEACDSLVDTVTNTWTLCGRPFMNSQ 180
QY 181 RAACICAEKEEKEEL 194
Db 181 RAACICAEKEEKEEL 194

RESULT 2
ADA41278
ID ADA41278 standard; protein; 194 AA.
XX ADA41278;
XX AC
XX 20-NOV-2003 (first entry)
XX DT
XX DE Human secreted protein.

XX Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnery; cardiant; gene therapy.

XX Homo sapiens.
OS WO3002102993-A2.
XX 27-DEC-2002.
XX 19-MAR-2002; 2002WO-US008123.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-175238/17.
XX New human secreted proteins and nucleic acid molecules, useful for
XX preparing a diagnostic or pharmaceutical composition for diagnosing,
XX preventing or treating cancer or other hyperproliferative disorder,
XX asthma, allergies or AIDS.
XX Claim 1; SEQ ID NO 1561; 3205pp; English.
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX treating or ameliorating medical conditions e.g. by protein or gene
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX fragments, and agonists or antagonists that bind to the polypeptide are
XX useful for preparing a diagnostic or pharmaceutical composition for
XX diagnosing or treating cancer or other hyperproliferative disorder. The
XX polypeptides and nucleic acid molecules are also useful for detecting,
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX or other hyperproliferative disorders including neoplasms, autoimmune
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX anaemia), haematopoietic or haematological disorders (e.g. anaemia,
XX thrombocytopenia), allergic reactions including asthma or eczema,
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX fungal or viral infections including HIV/AIDS), or wound healing and
XX disorders of epithelial cell proliferation. The nucleic acids are also
XX useful for chromosome identification, radiation hybrid mapping or long-
XX range restriction mapping, as molecular weight markers, or as
XX hybridization or diagnostic probes. The polypeptides and antibodies are
XX useful for providing immunological probes for differential identification
XX of the tissues immunohistochemistry assays. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 194 AA;
Query Match 99.5%; Score 193; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.7e-186;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLASGLFVLWLSGGGLAQSDDTSPDEESVSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGLFVLWLSGGGLAQSDDTSPDEESVSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
QY 61 NGVCQYCRYGKAPMPRGYKQPFNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
DB 61 NGVCQYCRYGKAPMPRGYKQPFNGCGSYFLGLKVPESMDLGPAMTKCCNQLDVCYD 120
QY 121 TCGANKYRCDAKFWCLXKSICSLKRSIGFVSKVEACDSLVDVTFTNTWTLGCRPFMNSQ 180
DB 121 TCGANKYRCDAKFWCLXKSICSLKRSIGFVSKVEACDSLVDVTFTNTWTLGCRPFMNSQ 180

QY 181 RAACICAEKEEKEEL 194
DB 181 RAACICAEKEEKEEL 194
RESULT 3
ABO13978
ID ABO13978 standard; protein; 194 AA.
XX ABO13978;
XX 21-AUG-2003 (first entry)
XX Novel human secreted protein #7.
XX Human; secreted protein; cytostatic; neuroprotective; hepatotropic;
XX gene therapy; cancer; liver disorder; hepatitis; neural disorder;
XX Alzheimer's disease.
XX Homo sapiens.
XX US2003028003-A1.
XX 06-FEB-2003.
XX 12-OCT-2001; 2001US-00974879.
XX 07-NOV-1997; 97US-0064900P.
XX 07-NOV-1997; 97US-0064908P.
XX 07-NOV-1997; 97US-0064911P.
XX 07-NOV-1997; 97US-0064912P.
XX 07-NOV-1997; 97US-0064983P.
XX 07-NOV-1997; 97US-0064984P.
XX 07-NOV-1997; 97US-0064985P.
XX 07-NOV-1997; 97US-0064987P.
XX 07-NOV-1997; 97US-0064988P.
XX 07-NOV-1997; 97US-0066089P.
XX 17-NOV-1997; 97US-0066090P.
XX 17-NOV-1997; 97US-0066094P.
XX 17-NOV-1997; 97US-0066095P.
XX 17-NOV-1997; 97US-0066100P.
XX 04-NOV-1998; 98WO-US023435.
XX 13-OCT-2000; 2000US-0239893P.
XX 28-MAR-2001; 2001US-00818683.
XX (ROSE/) ROSEN C A.
XX (FENG/) FENG P.
XX (RUBE/) RUBEN S M.
XX (EBNE/) EBNER R.
XX (OLSE/) OLSEN H S.
XX (NIJ/) NI J.
XX (WEI/) WEI Y.
XX (SOPE/) SOPPET D R.
XX (MOOR/) MOORE P A.
XX (KYAW/) KYAW H.
XX (LAFL/) LAFLEUR D W.
XX (SHIV/) SHI Y.
XX (JANA/) JANAT F.
XX (ENDR/) ENDRESS G A.
XX (CART/) CARTER K C.
XX (BIRS/) BIRSE C E.
XX Rosen CA, Feng P, Ruben SM, Ebner R, Olsen HS, Ni J, Wei Y;
XX Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;
XX Endress GA, Carter KC, Birse CE;
XX WPI; 2003-479549/45.
XX N-PSDB; ACD18865.
XX New nucleic acid molecule, useful for preparing a medicament for
XX preventing, treating or ameliorating a medical condition e.g., cancer,
XX liver disorders such as hepatitis or neural disorders such as Alzheimer's

PT disease.
XX PS Claim 11; Page 357; 496pp; English.
XX CC The invention describes a new isolated nucleic acid molecule comprising a
CC sequence having at least 95% identity with a sequence comprising: (a) a
CC polynucleotide (PN) fragment of a sequence comprising 420-3435 bp, or its
CC allelic variant; (b) a PN fragment of the cDNA sequence; (c) a PN
CC sequence encoding a polypeptide, or its fragment, domain, epitope or
CC species homologue; or (d) a PN that hybridises under stringent conditions
CC to any one of the sequences of (A)-(C). The nucleic acid is useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition e.g., cancer, liver disorders such as hepatitis or neural
CC disorders such as Alzheimer's disease. This is the amino acid sequence of
CC a novel human secreted protein
XX
XX Sequence 194 AA;
Query Match 99.5%; Score 193; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.7e-186;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 M K L A S G F L V L W L S L G G L A Q S D T S P D T E E S Y S D M G L R H L R G S F S V N S Y F D S F L E L L G G K 60
D b 1 M K L A S G F L V L W L S L G G L A Q S D T S P D T E E S Y S D M G L R H L R G S F S V N S Y F D S F L E L L G G K 60
QY 61 N G V C Q Y R C R Y G K A P M P R F G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
D b 61 N G V C Q Y R C R Y G K A P M P R F G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
QY 121 T C G A N K Y R C D A K F R W C L X S I C S D L K R S L G F V S K V E A C D S L V D T V F N T V T W T L G C R P F M N S Q 180
D b 121 T C G A N K Y R C D A K F R W C L X S I C S D L K R S L G F V S K V E A C D S L V D T V F N T V T W T L G C R P F M N S Q 180
QY 181 R A A C I C A E E E K E E L 194
D b 181 R A A C I C A E E E K E E L 194
RESULT 4
ID ABR48024
XX ABR48024 standard; protein; 194 AA.
AC ABR48024;
XX
DT 12-JUN-2003 (first entry)
DE Human secreted protein, SEQ ID 915.
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnery; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
OS Homo sapiens.
PN WO200295010-A2.
PD 28-NOV-2002.
PF 19-MAR-2002; 2002WO-US009785.
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM;
XX
PI WPI; 2003-129429/12.
XX
XX Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular

PT disorders such as arrhythmia.
XX PS Claim 13; SEQ ID NO 915; 1881pp; English.
XX CC The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACCS0344-ACCS0856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders, for
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 194 AA;
Query Match 99.5%; Score 193; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.7e-186;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 M K L A S G F L V L W L S L G G L A Q S D T S P D T E E S Y S D M G L R H L R G S F S V N S Y F D S F L E L L G G K 60
D b 1 M K L A S G F L V L W L S L G G L A Q S D T S P D T E E S Y S D M G L R H L R G S F S V N S Y F D S F L E L L G G K 60
QY 61 N G V C Q Y R C R Y G K A P M P R F G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
D b 61 N G V C Q Y R C R Y G K A P M P R F G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
QY 121 T C G A N K Y R C D A K F R W C L X S I C S D L K R S L G F V S K V E A C D S L V D T V F N T V T W T L G C R P F M N S Q 180
D b 121 T C G A N K Y R C D A K F R W C L X S I C S D L K R S L G F V S K V E A C D S L V D T V F N T V T W T L G C R P F M N S Q 180
QY 181 R A A C I C A E E E K E E L 194
D b 181 R A A C I C A E E E K E E L 194
RESULT 5
ID AAY27572
XX AAY27572 standard; protein; 195 AA.
AC AAY27572;
XX
DT 30-JUL-1999 (first entry)
DE Human secreted protein encoded by gene No. 6.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
XX WO9924836-A1.
PN

XX PD 20-MAY-1999.
 XX PF 04-NOV-1998; 98WO-US023435.
 XX PR 07-NOV-1997; 97US-0064900P.
 XX PR 07-NOV-1997; 97US-0064908P.
 XX PR 07-NOV-1997; 97US-0064911P.
 XX PR 07-NOV-1997; 97US-0064912P.
 XX PR 07-NOV-1997; 97US-0064983P.
 XX PR 07-NOV-1997; 97US-0064984P.
 XX PR 07-NOV-1997; 97US-0064985P.
 XX PR 07-NOV-1997; 97US-0064987P.
 XX PR 07-NOV-1997; 97US-0064988P.
 XX PR 07-NOV-1997; 97US-0066089P.
 XX PR 17-NOV-1997; 97US-0066090P.
 XX PR 17-NOV-1997; 97US-0066094P.
 XX PR 17-NOV-1997; 97US-0066095P.
 XX PR 17-NOV-1997; 97US-0066100P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA
 XX PI Feng P, Carter KC, Endress GA, Rosen CA, Ruben SM, Janat F;
 XX PI Ni J, Wei Y, Moore PA, Soppet DR, Kyaw H, Lafleur DW, Olsen HS;
 XX PI Shi Y, Ebner R;
 XX DR WPI; 1999-337740/28.
 XX DR N-PSDB; AAX84938.
 XX PT New human secreted proteins and coding sequences useful for treating
 XX PT disorders of the immune system and hyperproliferative disorders.
 XX PS
 XX PS Claim 11; Page 352-353; 507pp; English.
 XX CC This sequence represents a secreted human protein encoded by the gene
 XX CC clone detailed in the descriptor line. The gene can be used to generate
 XX CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 XX CC portion (e.g. AAX84924) for increasing the stability of the fused protein
 XX CC as compared to the human protein only. The invention relates to 125 novel
 XX CC genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino
 XX CC acid sequences AAY27567-Y27933) which are useful for preventing, treating
 XX CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 XX CC pathological conditions can be diagnosed by determining the amount of the
 XX CC new polypeptides in a sample or by determining the presence of mutations
 XX CC in the new polynucleotides. Specific uses are described for each of the
 XX CC 125 polynucleotides, based on which tissues they are most highly
 XX CC expressed in (see AAX84933 for described uses)
 XX CC
 XX CC Sequence 195 AA;
 XX CC
 XX CC Query Match 99.5%; Score 193; DB 2; Length 195;
 XX CC Best Local Similarity 100.0%; Pred. No. 3.7e-186; Indels 0; Gaps 0;
 XX CC Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M K L A S G F L V L W L S L G G G L A Q S D T S P D T E E S Y S D W G L R H L R G S F S V N S Y F D S F L L L G G K 60
 Db 1 M K L A S G F L V L W L S L G G G L A Q S D T S P D T E E S Y S D W G L R H L R G S F S V N S Y F D S F L L L G G K 60
 QY 61 N G V C Q Y R C R Y K A P M P R P G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
 Db 61 N G V C Q Y R C R Y K A P M P R P G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
 QY 121 T C G A N K Y R C D A K F R W C L 194
 Db 121 T C G A N K Y R C D A K F R W C L 194
 QY 181 R A A C I C A E E K E E L 194
 Db 181 R A A C I C A E E K E E L 194
 RESULT 6
 ABP62920

ID XX ABP62920 standard; protein; 194 AA.
 AC XX ABP62920;
 XX DT 14-OCT-2002 (first entry)
 XX XX Human polypeptide SEQ ID NO 357.
 DE XX
 XX Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 XX OS Homo sapiens.
 XX XX WO200218424-A2.
 PN 07-MAR-2002.
 PD 31-AUG-2001; 2001WO-US027093.
 PF 01-SEP-2000; 2000US-00654935.
 PR (HYSE-) HYSEQ INC.
 XX PA
 XX PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 XX PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
 XX DR WPI; 2002-583321/62.
 XX DR N-PSDB; ABQ93399.
 XX PT New polynucleotide and polypeptides, useful for treatment and diagnosis
 XX PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 XX PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 XX PT sclerosis, diabetes and allergies.
 XX PS Claim 20; SEQ ID NO 357; 284pp + Sequence Listing; English.
 XX CC The invention relates to an isolated polynucleotide (I) comprising one of
 XX CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
 XX CC administering to a mammalian subject a composition comprising the protein
 XX CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 XX CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 XX CC (I) is useful for gene therapy of diseases and (II) can be used for
 XX CC therapeutic treatment. Diseases that may be treated include wound healing
 XX CC and tissue repair, burns, central nervous system disorders (e.g.
 XX CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 XX CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 XX CC sclerosis, diabetes and allergies. Note: The sequence data for this
 XX CC patent did not form part of the printed specification, but was obtained
 XX CC in electronic format directly from WIPO at
 XX CC ftp.wipo.int/pub/published_pct_sequences
 XX CC
 XX CC Sequence 194 AA;
 XX CC
 XX CC Query Match 70.6%; Score 137; DB 5; Length 194;
 XX CC Best Local Similarity 100.0%; Pred. No. 1.1e-129;
 XX CC Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M K L A S G F L V L W L S L G G G L A Q S D T S P D T E E S Y S D W G L R H L R G S F S V N S Y F D S F L L L G G K 60
 Db 1 M K L A S G F L V L W L S L G G G L A Q S D T S P D T E E S Y S D W G L R H L R G S F S V N S Y F D S F L L L G G K 60
 QY 61 N G V C Q Y R C R Y K A P M P R P G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
 Db 61 N G V C Q Y R C R Y K A P M P R P G Y K P Q E P N G C G S Y F L G L K V P E S M D L G I P A M T K C N Q L D V C Y D 120
 QY 121 T C G A N K Y R C D A K F R W C L 137
 Db 121 T C G A N K Y R C D A K F R W C L 137

CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 194 AA;

Query Match 70.6%; Score 137; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.le-129;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSFESVNSYFDSFLELLGK 60
DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHRLGSFESVNSYFDSFLELLGK 60

QY 61 NGVCQYRCRYGKAPMRPRGYKPOEPNGCGSYFLGLKVPEMDLGPAMTKCCNQLDVCYD 120
DB 61 NGVCQYRCRYGKAPMRPRGYKPOEPNGCGSYFLGLKVPEMDLGPAMTKCCNQLDVCYD 120

QY 121 TCGANKYRCDAKFRWCL 137
DB 121 TCGANKYRCDAKFRWCL 137

RESULT 8
ADA40769
ID ADA40769 standard; protein; 194 AA.
XX
AC ADA40769;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; neutropenic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnary; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
PN W02002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
WPI; 2003-167512/16.
XX
N-PSDB; ADA56025.
XX
New human secreted polypeptides and polynucleotides, useful for
diagnosing, treating or preventing e.g. immune disorders, inflammatory
conditions, respiratory disorders, cancers, CNS disorders, or
neurodegenerative disorders.
XX
Claim 13; SEQ ID NO 1111; 1754pp; English.
XX
The invention relates to 592 new human secreted polypeptides useful for
diagnosing, treating or preventing e.g. immune disorders, inflammatory
conditions, respiratory disorders, cancers, CNS disorders, or
neurodegenerative disorders, or polypeptides comprising an amino acid
sequence at least 95% identical to the new sequences. The polypeptides,
antibodies or antibody fragments that bind to the polypeptides, nucleic
acids encoding the polypeptides, agonists or antagonists that binds to
the polypeptide, are useful in preparing diagnostic or pharmaceutical
compositions for diagnosing, treating or preventing an e.g. immune
disorders, inflammatory conditions (e.g. inflammatory bowel disease,
nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
(e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
disorders (e.g. Parkinson's disease or Alzheimer's disease), and
cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
polynucleotides are useful for chromosome identification, chromosome
mapping, for controlling gene expression through triple helix formation
or antisense DNA or RNA, in gene therapy, for identifying individuals
from minute biological samples, in forensic biology, and as hybridization
probes. The polypeptides are useful for as molecular weight markers on
sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
gels, to raise antibodies, for testing biological activities, and for
treating or preventing neural disorders, immune system disorders,
muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
renal, proliferative and/or cancerous diseases. This sequence corresponds
to one of the polypeptide of the invention. Note: The sequence data for

preventing, diagnosing, prognosticating, treating or ameliorating cancer or other hyperproliferative disorders including neoplasms, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematological disorders (e.g. anaemia, thrombocytopenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory bowel disease or Crohn's disease), neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), infectious diseases (bacterial, fungal or viral infections including HIV/AIDS), or wound healing and disorders of epithelial cell proliferation. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 70.6%; Score 137; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.1e-129;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRGYKQBPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRGYKQBPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120

QY 121 TCGANKYRCDAKFRWCL 137
DB 121 TCGANKYRCDAKFRWCL 137

RESULT 9
ID ABR47739 standard; protein; 194 AA.
XX ABR47739;
AC ABR47739;
XX 12-JUN-2003 (first entry)
XX Human secreted protein, SEQ ID 630.
DE Cardiant; antiarrhythmic; antiarteriosclerotic; vasotrophic; cytostatic;
XX vulnary; antiinflammatory; nootropic; neuroprotective;
XX antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX Homo sapiens.
XX WO200295010-A2.
XX 28-NOV-2002.
XX 19-MAR-2002; 2002WO-US009785.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-129429/12.
XX Novel human secreted proteins, useful for detecting, preventing,

diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
Claim 13; SEQ ID NO 630; 1881bp; English.
The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue disease, to enhance bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 70.6%; Score 137; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.1e-129;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60
DB 1 MKLASGFLVLSLGGGLAQSDTSPDTEESYSDWGLRHLRGSFESVNSYFDSFLELLGGK 60

QY 61 NGVCQYRCRYGKAPMPRGYKQBPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120
DB 61 NGVCQYRCRYGKAPMPRGYKQBPNGCGSYFLGLKVPESMDLGPAMTKCNQLDVCYD 120

QY 121 TCGANKYRCDAKFRWCL 137
DB 121 TCGANKYRCDAKFRWCL 137

RESULT 10
ID ADE08422 standard; protein; 335 AA.
XX ADE08422;
XX 29-JAN-2004 (first entry)
XX Novel protein (useful for identifying genetic disorders) #577.
XX novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder.
XX Unidentified.
XX WO2003054152-A2.
XX 03-JUL-2003.
XX 10-DEC-2002; 2002WO-US039555.
XX 10-DEC-2001; 2001US-0339739P.
XX 11-DEC-2001; 2001US-0339453P.
XX 14-MAR-2002; 2002US-0365091P.
XX 14-MAR-2002; 2002US-0365384P.

Mon May 17 11:51:01 2004

DNA encoding allergens of Cladosporium herbarum - useful for diagnosis and treatment of allergy.

Claim 7; Page 11; 20pp; German.

AAR99963-65 are B-cell epitopes of Cladosporium herbarum allergen, Clah12 (AAR99961). Clah12 and its fragments are useful in diagnosis and therapy, esp. in vitro detection of allergy to Clah8/12 by reactivity with serum IgE or cellular reaction to these allergens. Therapeutically they may stimulate proliferation and interleukin prod. in T cells, in vitro or in vivo, and also block T cells (induce tolerance of allergen-specific T cells). The use of allergen-deriv. but non-anaphylactic peptides allows larger doses to be admin. improving hypersensitisation therapy. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 19 AA;

Query Match 3.6%; Score 7; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
DB 7 ABEKEE 13

RESULT 13
AAR72674 AAR72674 standard; peptide; 23 AA.

AC AAR72674;
XX 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 25-OCT-1995 (first entry)
XX Cladosporium herbarum allergen Clah11 B-cell epitope (85-107).
XX Fungal spore; allergen; Clah11; allergy; ribosomal protein; RLA2;
KW B-cell epitope; antigenic region.

XX Davidiella tassiana.

XX WO9506121-A2.

XX 02-MAR-1995.

XX 24-AUG-1994; 94WO-AT000120.

XX 27-AUG-1993; 93AT-00001725.

XX (BIOM-) BIOMAY PROD & HANDELSGES MEH.

XX Achatz G, Oberkofler H, Simon B, Unger A, Lechenauer E;

PI Hirschwehr R, Ebner C, Kraft D, Prillinger H, Breitenbach M;

XX WPI; 1995-106850/14.

XX Allergens derived from Cladosporium herbarum spores - also recombinant DNA for expressing the allergens, useful for in vitro allergy detection.

XX Claim 1; Page 27; 35pp; German.

XX Spores of Cladosporium herbarum are the most common fungal spores found in the air; they can cause allergic reactions. Various Clah allergens and sequences encoding them have now been isolated. The mature Clah11 allergen has mol. wt. 11 kD and is encoded by cDNA sequence AAQ87846. The allergen has homology to the ribosomal protein RLA2. Potential epitopic subfragments were identified by computer analysis of the amino acid sequence. See AAR72670-R72674 for potential B-cell epitopes and AAR72675-R72677 for potential T-cell epitopes. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

SQ Sequence 23 AA;

Query Match 3.6%; Score 7; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
DB 10 ABEKEE 16

RESULT 14
ADB48041 ADB48041 standard; protein; 34 AA.

XX AC ADB48041;
XX 04-DEC-2003 (first entry)
DT Novel human secreted protein associated polypeptide #120.
DE human; secreted protein; insulin; haemoglobin S; haemoglobin B;
KW superoxide; SOD; catalase; DNA repair protein; oncogene;
KW tumour suppressor; tumour necrosis factor; TNF; inflammation;
KW blood vessel growth inhibition; immune response; immune system disorder;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW peripheral artery disease; limb ischaemia; arterio-arterial fistula;
KW arteriovenous fistula; congenital heart defect;
KW neovascularisation disorder; wound healing;
KW epithelial cell proliferation; neurological disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; mania; dementia;
KW infectious disease.

XX Homo sapiens.

XX US2003054443-A1.

XX 20-MAR-2003.

XX 04-OCT-2001; 2001US-00969730.

XX 05-AUG-1997; 97US-0054798P.

XX 05-AUG-1997; 97US-0054803P.

XX 05-AUG-1997; 97US-0054804P.

XX 05-AUG-1997; 97US-0054806P.

XX 05-AUG-1997; 97US-0054807P.

XX 05-AUG-1997; 97US-0054808P.

XX 05-AUG-1997; 97US-0054809P.

XX 05-AUG-1997; 97US-0055309P.

XX 05-AUG-1997; 97US-0055310P.

XX 05-AUG-1997; 97US-0055311P.

XX 05-AUG-1997; 97US-0055312P.

XX 18-AUG-1997; 97US-0055386P.

XX 18-AUG-1997; 97US-0055970P.

XX 18-AUG-1997; 97US-0055986P.

XX 19-AUG-1997; 97US-0056364P.

XX 19-AUG-1997; 97US-0056365P.

XX 19-AUG-1997; 97US-0056366P.

XX 19-AUG-1997; 97US-0056367P.

XX 19-AUG-1997; 97US-0056370P.

XX 19-AUG-1997; 97US-0056371P.

XX 19-AUG-1997; 97US-0056557P.

XX 19-AUG-1997; 97US-0056731P.

XX 19-AUG-1997; 97US-0056732P.

XX 04-AUG-1998; 98WO-US016235.

XX 04-FEB-1999; 99US-00244112.

XX 06-OCT-2000; 2000US-0238291P.

XX 01-FEB-2001; 2001US-00774639.

XX (RUBE/) RUBEN S M.

XX (SOPP/) SOPPET D R.

XX (EBNE/) EBNER R.

Mon May 17 11:51:01 2004

25-MAR-2003 (revised)
 26-JUN-1995 (first entry)
 M.kandleri topoisomerase V proteolytic fragment.
 TI; supercoiled DNA; relaxing; closed circular DNA; sequencing; cloning;
 amplification; probe.
 Methanopyrus kandleri.
 WO9421811-A1.
 29-SEP-1994.
 24-MAR-1994; 94WO-US003217.
 24-MAR-1993; 93US-00038343.
 (SLES/) SLESAREV A I.
 Slesarev AI;
 WPI; 1994-317030/39.
 New thermostable DNA topoisomerase - obtd. from Methanopyrus kandleri,
 used for relaxing supercoiled DNA and unlinking closed circular DNA.
 Claim 10; Page 70; 104pp; English.
 The sequence is that of a proteolytic fragment of a new topoisomerase
 (TI) from Methanopyrus kandleri. The TI is a type I-group B TI whose
 reaction proceeds via a transient single stranded break which changes the
 linking number in steps of one and operates on duplex DNA. The TI can be
 used for relaxing supercoiled DNA or for unlinking closed circular DNA.
 See also AAR60684-90. (Updated on 25-MAR-2003 to correct PN field.)
 Query Match 3.6%; Score 7; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194
 Db 10 EEEKEEL 16
 Search completed: May 17, 2004, 10:51:41
 Job time : 111 secs

(OLSE/) OLSEN H S.
 (YOUN/) YOUNG P E.
 (GREE/) GREENE J M.
 (FERR/) FERRIE A M.
 (YUGG/) YU G.
 (NIJJ/) NI J.
 (ROSE/) ROSEN C A.
 (BREM/) BREWER L A.
 (JANA/) JANAT F.
 (BIRS/) BIRSE C E.
 Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;
 Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F, Birse CE;
 WPI; 2003-695903/66.
 Novel human secreted proteins useful for treating and/or diagnosing
 disorders of immune system, cardiovascular disorders such as peripheral
 artery disease, neurological diseases such as Alzheimer's disease.
 Disclosure; Page 54; 333pp; English.

The invention relates to novel human secreted proteins. The protein is
 useful for preventing, treating or ameliorating a medical condition. The
 protein is useful for diagnosing a pathological condition or
 susceptibility to a pathological condition in a subject. The protein is
 useful for identifying a binding partner. The nucleic acid is useful for
 diagnosing pathological condition or a susceptibility to pathological
 condition in a subject. The protein is useful as reagents for
 differential identification of the tissues or cell types present in a
 biological sample. The protein can be administered to patients having
 absent or decreased levels of polypeptides e.g. insulin, to supplement
 absent or decreased levels of different polypeptides, e.g. haemoglobin S
 for haemoglobin B, superoxide (SOD), catalase, DNA repair protein, to
 inhibit the activity of a polypeptide e.g. an oncogene or tumour
 suppressor, to activate the activity of polypeptide e.g. by binding to a
 receptor, to reduce the activity of membrane bound receptor by competing
 with it for free ligand e.g. soluble tumour necrosis factor (TNF)
 receptors used in reducing inflammation, or to bring about a desired
 response e.g. blood vessel growth inhibition, enhancement of immune
 acid are useful for treating, preventing, detecting, diagnosing disorders
 of immune system involving abnormal growth of specific types of cells as
 well as of other cell types where expression has been observed. The
 protein, the nucleic acid and antibodies are useful for treating,
 preventing and/or diagnosing diseases, disorders and/or conditions of
 immune system, hyperproliferative disorders including neoplasms,
 cardiovascular disorders (such as peripheral artery disease, limb
 ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital
 heart defects, etc), neovascularisation disorders, wound healing and
 epithelial cell proliferation, neurological diseases (such as Alzheimer's
 disease, Parkinson's disease, Huntington's disease, mania, dementia,
 etc), infectious diseases caused by virus, bacteria, fungi, etc. The
 present sequence represents the amino acid sequence of a novel human
 secreted protein associated polypeptide.

Sequence 34 AA;
 Query Match 3.6%; Score 7; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LWLSLGG 16
 Db 2 LWLSLGG 8

RESULT 15
 AAR60689
 ID AAR60689 standard; protein; 35 AA.
 XX
 AC AAR60689;
 XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:49:45 ; Search time 23 Seconds
(without alignments)
435.454 Million cell updates/sec

Title: US-10-621-401-145
Perfect score: 194
Sequence: 1 MKLASGLVWLWLSGGGLAQ.....PFMNSORACICAEKEEL 194

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 8 | 4.1 | 214 | 1 | US-08-155-171B-16 |
| 2 | 8 | 4.1 | 214 | 2 | US-08-435-998-16 |
| 3 | 7 | 3.6 | 35 | 1 | US-08-038-343A-5 |
| 4 | 7 | 3.6 | 106 | 1 | US-08-185-414E-4 |
| 5 | 7 | 3.6 | 144 | 4 | US-09-250-609-2 |
| 6 | 7 | 3.6 | 144 | 4 | US-09-250-611-2 |
| 7 | 7 | 3.6 | 176 | 4 | US-09-216-393B-73 |
| 8 | 7 | 3.6 | 191 | 4 | US-09-134-000C-3705 |
| 9 | 7 | 3.6 | 204 | 2 | US-08-715-204-1 |
| 10 | 7 | 3.6 | 204 | 2 | US-08-691-814B-10 |
| 11 | 7 | 3.6 | 204 | 3 | US-09-162-597-1 |
| 12 | 7 | 3.6 | 204 | 4 | US-09-250-609-4 |
| 13 | 7 | 3.6 | 204 | 4 | US-09-250-609-9 |
| 14 | 7 | 3.6 | 204 | 4 | US-09-250-611-4 |
| 15 | 7 | 3.6 | 204 | 4 | US-09-250-611-9 |
| 16 | 7 | 3.6 | 264 | 4 | US-09-540-236-2978 |
| 17 | 7 | 3.6 | 320 | 4 | US-09-848-739-6 |
| 18 | 7 | 3.6 | 320 | 4 | US-09-818-739-7 |
| 19 | 7 | 3.6 | 359 | 4 | US-09-071-035-472 |
| 20 | 7 | 3.6 | 388 | 4 | US-09-252-991A-27381 |
| 21 | 7 | 3.6 | 396 | 3 | US-08-961-083-16 |
| 22 | 7 | 3.6 | 396 | 4 | US-09-536-784-16 |
| 23 | 7 | 3.6 | 434 | 3 | US-08-111-939-13 |
| 24 | 7 | 3.6 | 434 | 3 | US-09-233-989-7 |
| 25 | 7 | 3.6 | 435 | 1 | US-08-111-939-14 |
| 26 | 7 | 3.6 | 435 | 1 | US-08-111-939-15 |
| 27 | 7 | 3.6 | 435 | 1 | US-08-111-939-16 |
| 1 | 8 | 4.1 | 214 | 1 | US-08-155-171B-16 |
| 2 | 8 | 4.1 | 214 | 2 | US-08-435-998-16 |
| 3 | 7 | 3.6 | 35 | 1 | US-08-038-343A-5 |
| 4 | 7 | 3.6 | 106 | 1 | US-08-185-414E-4 |
| 5 | 7 | 3.6 | 144 | 4 | US-09-250-609-2 |
| 6 | 7 | 3.6 | 144 | 4 | US-09-250-611-2 |
| 7 | 7 | 3.6 | 176 | 4 | US-09-216-393B-73 |
| 8 | 7 | 3.6 | 191 | 4 | US-09-134-000C-3705 |
| 9 | 7 | 3.6 | 204 | 2 | US-08-715-204-1 |
| 10 | 7 | 3.6 | 204 | 2 | US-08-691-814B-10 |
| 11 | 7 | 3.6 | 204 | 3 | US-09-162-597-1 |
| 12 | 7 | 3.6 | 204 | 4 | US-09-250-609-4 |
| 13 | 7 | 3.6 | 204 | 4 | US-09-250-609-9 |
| 14 | 7 | 3.6 | 204 | 4 | US-09-250-611-4 |
| 15 | 7 | 3.6 | 204 | 4 | US-09-250-611-9 |
| 16 | 7 | 3.6 | 264 | 4 | US-09-540-236-2978 |
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| 19 | 7 | 3.6 | 359 | 4 | US-09-071-035-472 |
| 20 | 7 | 3.6 | 388 | 4 | US-09-252-991A-27381 |
| 21 | 7 | 3.6 | 396 | 3 | US-08-961-083-16 |
| 22 | 7 | 3.6 | 396 | 4 | US-09-536-784-16 |
| 23 | 7 | 3.6 | 434 | 3 | US-08-111-939-13 |
| 24 | 7 | 3.6 | 434 | 3 | US-09-233-989-7 |
| 25 | 7 | 3.6 | 435 | 1 | US-08-111-939-14 |
| 26 | 7 | 3.6 | 435 | 1 | US-08-111-939-15 |
| 27 | 7 | 3.6 | 435 | 1 | US-08-111-939-16 |

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| 28 | 7 | 3.6 | 435 | 1 | US-08-452-262-2 | Sequence 2, Appli |
| 29 | 7 | 3.6 | 435 | 1 | US-08-734-550-2 | Sequence 2, Appli |
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| 34 | 7 | 3.6 | 476 | 3 | US-09-233-989-6 | Sequence 6, Appli |
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| 36 | 7 | 3.6 | 497 | 1 | US-08-633-485-6 | Sequence 5, Appli |
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| 47 | 7 | 3.6 | 962 | 4 | US-09-071-035-250 | Sequence 250, App |
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| 51 | 7 | 3.6 | 962 | 4 | US-09-071-035-478 | Sequence 478, App |
| 52 | 7 | 3.6 | 970 | 4 | US-09-134-000C-5691 | Sequence 5691, App |
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| 54 | 6 | 3.1 | 9 | 4 | US-09-285-630-7 | Sequence 7, Appli |
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| 57 | 6 | 3.1 | 29 | 4 | US-09-205-258-823 | Sequence 823, App |
| 58 | 6 | 3.1 | 29 | 4 | US-09-205-258-1090 | Sequence 1090, Ap |
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| 60 | 6 | 3.1 | 71 | 4 | US-08-311-731A-388 | Sequence 388, App |
| 61 | 6 | 3.1 | 71 | 4 | US-09-543-681A-7079 | Sequence 7079, Ap |
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| 63 | 6 | 3.1 | 75 | 4 | US-09-621-976-7640 | Sequence 7640, Ap |
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| 69 | 6 | 3.1 | 85 | 3 | US-08-772-440-36 | Sequence 326, App |
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| 71 | 6 | 3.1 | 91 | 4 | US-09-345-236B-132 | Sequence 5832, Ap |
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| 84 | 6 | 3.1 | 127 | 4 | US-09-252-991A-20663 | Sequence 23, Appli |
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| 86 | 6 | 3.1 | 131 | 3 | US-08-772-440-27 | Sequence 16, Appli |
| 87 | 6 | 3.1 | 134 | 3 | US-08-772-440-16 | Sequence 14, Appli |
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| 95 | 6 | 3.1 | 168 | 4 | US-09-107-532A-6863 | Sequence 1150, Ap |
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| 112 | 6 | 3.1 | 209 | 3 | US-09-252-991A-31712 | Sequence 4, Appl | 185 | 3.1 | 330 | 3 | US-08-854-050-203 | Sequence 203, App |
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| 114 | 6 | 3.1 | 212 | 3 | US-08-861-774E-42 | Sequence 42, Appl | 187 | 3.1 | 330 | 4 | US-09-402-181B-322 | Sequence 322, App |
| 115 | 6 | 3.1 | 214 | 3 | US-09-717-364A-17 | Sequence 17, Appl | 188 | 3.1 | 330 | 4 | US-09-721-456-332 | Sequence 322, App |
| 116 | 6 | 3.1 | 218 | 3 | US-09-154-874-2 | Sequence 2, Appl | 189 | 3.1 | 334 | 2 | US-08-566-096A-6 | Sequence 6, Appl |
| 117 | 6 | 3.1 | 218 | 4 | US-08-931-668-2 | Sequence 2, Appl | 190 | 3.1 | 334 | 2 | US-08-668-650B-6 | Sequence 6, Appl |
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| 125 | 6 | 3.1 | 230 | 2 | US-08-537-400-16 | Sequence 16, Appl | 198 | 3.1 | 338 | 4 | US-09-312-283C-325 | Sequence 92, Appl |
| 126 | 6 | 3.1 | 230 | 2 | US-08-706-702-18 | Sequence 18, Appl | 199 | 3.1 | 341 | 2 | US-08-846-762-92 | Sequence 33006, A |
| 127 | 6 | 3.1 | 230 | 2 | US-08-706-702-18 | Sequence 18, Appl | 200 | 3.1 | 347 | 4 | US-09-252-991A-31325 | Sequence 31325, A |
| 128 | 6 | 3.1 | 230 | 4 | US-09-238-471-18 | Sequence 18, Appl | 201 | 3.1 | 352 | 4 | US-08-713-636-2 | Sequence 2, Appl |
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| 130 | 6 | 3.1 | 237 | 4 | US-09-482-273-198 | Sequence 198, App | 203 | 3.1 | 360 | 4 | US-09-120-365-75 | Sequence 75, Appl |
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| 133 | 6 | 3.1 | 240 | 3 | US-08-559-397A-14 | Sequence 14, Appl | 206 | 3.1 | 371 | 4 | US-09-252-991A-23727 | Sequence 1, Appl |
| 134 | 6 | 3.1 | 240 | 3 | US-08-559-397A-14 | Sequence 46, Appl | 207 | 3.1 | 384 | 4 | US-08-935-887-1 | Sequence 36, Appl |
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| 141 | 6 | 3.1 | 267 | 4 | US-09-172-699-18 | Sequence 6058, Ap | 214 | 3.1 | 415 | 2 | US-07-667-276A-4 | Sequence 4, Appl |
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| 146 | 6 | 3.1 | 297 | 1 | US-08-077-673-6 | Sequence 6, Appl | 219 | 3.1 | 422 | 4 | US-08-705-771-16 | Sequence 16, Appl |
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| 158 | 6 | 3.1 | 315 | 4 | US-09-674-529B-6 | Sequence 6, Appl | 231 | 3.1 | 436 | 4 | US-07-870-985A-17 | Sequence 17, Appl |
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| 165 | 6 | 3.1 | 327 | 1 | US-08-240-049B-14 | Sequence 14, Appl | 238 | 3.1 | 440 | 2 | US-09-634-238-281 | Sequence 281, App |
| 166 | 6 | 3.1 | 327 | 1 | US-08-259-148A-15 | Sequence 15, Appl | 239 | 3.1 | 440 | 4 | US-09-252-991A-22913 | Sequence 22913, A |
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| 173 | 6 | 3.1 | 327 | 3 | US-08-542-634-17 | Sequence 17, Appl | 246 | 3.1 | 445 | 2 | US-08-630-118A-4 | Sequence 4, Appl |

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| 261 | 6 | 3.1 | 445 | 4 | US-09-327-035-6 | Sequence 6, Appli | 334 | 6 | 3.1 | 567 | 4 | US-09-957-960-2 | Sequence 2, Appli |
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| 266 | 6 | 3.1 | 455 | 2 | US-08-566-096A-4 | Sequence 4, Appli | 339 | 6 | 3.1 | 571 | 5 | PCT-US96-09641-37 | Sequence 37, Appl |
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| 268 | 6 | 3.1 | 455 | 2 | US-09-200-673-4 | Sequence 4, Appli | 341 | 6 | 3.1 | 578 | 3 | US-08-484-661A-11 | Sequence 11, Appl |
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| 270 | 6 | 3.1 | 455 | 4 | US-09-1013-946-7 | Sequence 7, Appli | 343 | 6 | 3.1 | 578 | 5 | PCT-US96-09641-11 | Sequence 11, Appl |
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| 272 | 6 | 3.1 | 455 | 4 | US-08-349-025-2 | Sequence 2, Appli | 345 | 6 | 3.1 | 593 | 1 | US-08-296-362-2 | Sequence 8, Appli |
| 273 | 6 | 3.1 | 456 | 1 | US-08-349-025-2 | Sequence 2, Appli | 346 | 6 | 3.1 | 603 | 4 | US-09-396-149-8 | Sequence 32874, A |
| 274 | 6 | 3.1 | 456 | 2 | US-08-566-096A-2 | Sequence 2, Appli | 347 | 6 | 3.1 | 606 | 4 | US-09-252-991A-22263 | Sequence 22263, A |
| 275 | 6 | 3.1 | 456 | 2 | US-08-668-650B-2 | Sequence 2, Appli | 348 | 6 | 3.1 | 606 | 4 | US-09-252-991A-22263 | Sequence 8, Appli |
| 276 | 6 | 3.1 | 456 | 2 | US-09-200-673-2 | Sequence 2, Appli | 349 | 6 | 3.1 | 610 | 3 | US-08-484-661A-16 | Sequence 16, Appl |
| 277 | 6 | 3.1 | 456 | 4 | US-03-194-895-2 | Sequence 2, Appli | 350 | 6 | 3.1 | 610 | 3 | US-08-484-661A-19 | Sequence 19, Appl |
| 278 | 6 | 3.1 | 456 | 4 | US-03-194-895-14 | Sequence 14, Appli | 351 | 6 | 3.1 | 610 | 3 | US-08-484-661A-23 | Sequence 23, Appl |
| 279 | 6 | 3.1 | 456 | 4 | US-09-447-907-2 | Sequence 2, Appli | 352 | 6 | 3.1 | 610 | 3 | US-08-484-661A-26 | Sequence 26, Appl |
| 280 | 6 | 3.1 | 456 | 4 | US-09-447-907-14 | Sequence 14, Appli | 353 | 6 | 3.1 | 610 | 3 | US-08-484-661A-29 | Sequence 29, Appl |
| 281 | 6 | 3.1 | 456 | 5 | PCT-US95-15646-2 | Sequence 2, Appli | 354 | 6 | 3.1 | 610 | 3 | US-08-484-661A-33 | Sequence 33, Appl |
| 282 | 6 | 3.1 | 456 | 5 | PCT-US95-15646-4 | Sequence 4, Appli | 355 | 6 | 3.1 | 610 | 3 | US-08-484-661A-35 | Sequence 35, Appl |
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| 284 | 6 | 3.1 | 463 | 4 | US-09-134-000C-4873 | Sequence 4873, Ap | 357 | 6 | 3.1 | 610 | 3 | US-08-656-664-16 | Sequence 16, Appl |
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| 287 | 6 | 3.1 | 470 | 3 | US-08-068-392-2 | Sequence 2, Appli | 360 | 6 | 3.1 | 610 | 3 | US-08-656-664-33 | Sequence 33, Appl |
| 288 | 6 | 3.1 | 470 | 3 | US-08-396-988-2 | Sequence 2, Appli | 361 | 6 | 3.1 | 610 | 3 | US-08-656-664-35 | Sequence 35, Appl |
| 289 | 6 | 3.1 | 470 | 3 | US-09-391-104-26 | Sequence 26, Appl | 362 | 6 | 3.1 | 610 | 3 | US-08-656-664-4 | Sequence 4, Appli |
| 290 | 6 | 3.1 | 476 | 3 | US-09-306-593-9 | Sequence 9, Appli | 363 | 6 | 3.1 | 610 | 3 | US-09-019-160-4 | Sequence 10, Appl |
| 291 | 6 | 3.1 | 477 | 4 | US-09-252-991A-22197 | Sequence 22197, A | 364 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-8 | Sequence 8, Appli |
| 292 | 6 | 3.1 | 479 | 3 | US-09-446-504-64 | Sequence 64, Appl | 365 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-16 | Sequence 16, Appl |
| 293 | 6 | 3.1 | 479 | 3 | US-09-712-266-64 | Sequence 39, Appl | 366 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-19 | Sequence 19, Appl |
| 294 | 6 | 3.1 | 494 | 3 | US-08-484-661A-39 | Sequence 39, Appl | 367 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-23 | Sequence 23, Appl |
| 295 | 6 | 3.1 | 494 | 3 | US-08-656-664-39 | Sequence 39, Appl | 368 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-26 | Sequence 26, Appl |
| 296 | 6 | 3.1 | 494 | 5 | PCT-US96-09641-39 | Sequence 13, Appl | 369 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-29 | Sequence 29, Appl |
| 297 | 6 | 3.1 | 500 | 4 | US-09-265-630-13 | Sequence 24948, A | 370 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-33 | Sequence 33, Appl |
| 298 | 6 | 3.1 | 502 | 4 | US-09-252-991A-24948 | Sequence 24948, A | 371 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-35 | Sequence 35, Appl |
| 299 | 6 | 3.1 | 502 | 4 | US-09-252-991A-28736 | Sequence 28736, A | 372 | 6 | 3.1 | 610 | 3 | PCT-US96-09641-54 | Sequence 54, Appl |
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| 301 | 6 | 3.1 | 503 | 3 | US-09-323-998B-61 | Sequence 61, Appl | 374 | 6 | 3.1 | 611 | 4 | US-09-252-991A-19134 | Sequence 19134, A |
| 302 | 6 | 3.1 | 503 | 3 | US-08-857-076-46 | Sequence 46, Appl | 375 | 6 | 3.1 | 612 | 4 | US-08-295-814B-4 | Sequence 4, Appli |
| 303 | 6 | 3.1 | 509 | 3 | US-08-974-549A-605 | Sequence 605, App | 376 | 6 | 3.1 | 612 | 4 | US-08-291-299-10 | Sequence 10, Appl |
| 304 | 6 | 3.1 | 514 | 3 | US-08-912-951-319 | Sequence 319, App | 377 | 6 | 3.1 | 627 | 1 | US-09-143-361-4 | Sequence 4, Appli |
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| 306 | 6 | 3.1 | 514 | 4 | US-09-107-532A-6217 | Sequence 6217, Ap | 379 | 6 | 3.1 | 627 | 3 | US-08-973-462-9 | Sequence 9, Appli |
| 307 | 6 | 3.1 | 522 | 4 | US-08-542-634-27 | Sequence 27, Appl | 380 | 6 | 3.1 | 627 | 5 | PCT-US95-10579-10 | Sequence 10, Appl |
| 308 | 6 | 3.1 | 525 | 3 | US-08-542-634-28 | Sequence 28, Appl | 381 | 6 | 3.1 | 627 | 5 | PCT-US95-10579-10 | Sequence 10, Appl |
| 309 | 6 | 3.1 | 525 | 3 | PCT-US95-13703-27 | Sequence 27, Appl | 382 | 6 | 3.1 | 627 | 5 | PCT-US95-10579-10 | Sequence 10, Appl |
| 310 | 6 | 3.1 | 525 | 3 | US-08-542-634-28 | Sequence 28, Appl | 383 | 6 | 3.1 | 627 | 5 | PCT-US95-10579-10 | Sequence 10, Appl |
| 311 | 6 | 3.1 | 525 | 5 | PCT-US95-13703-28 | Sequence 28, Appl | 384 | 6 | 3.1 | 630 | 3 | US-08-295-814B-10 | Sequence 10, Appl |
| 312 | 6 | 3.1 | 528 | 4 | US-09-010-147B-20 | Sequence 20, Appl | 385 | 6 | 3.1 | 632 | 3 | US-09-143-361-10 | Sequence 10, Appl |
| 313 | 6 | 3.1 | 533 | 4 | US-09-107-532A-6006 | Sequence 6006, Ap | 386 | 6 | 3.1 | 632 | 3 | PCT-US93-01959-10 | Sequence 10, App |
| 314 | 6 | 3.1 | 537 | 4 | US-09-489-039A-12290 | Sequence 12290, A | 387 | 6 | 3.1 | 632 | 5 | US-08-857-076-101 | Sequence 101, App |
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| 316 | 6 | 3.1 | 540 | 3 | US-08-542-634-25 | Sequence 25, Appl | 389 | 6 | 3.1 | 636 | 4 | US-09-252-991A-21770 | Sequence 95, Appl |
| 317 | 6 | 3.1 | 540 | 3 | US-08-542-634-26 | Sequence 26, Appl | 390 | 6 | 3.1 | 638 | 2 | US-08-846-762-95 | Sequence 2, Appli |
| 318 | 6 | 3.1 | 540 | 3 | US-08-542-634-25 | Sequence 25, Appl | 391 | 6 | 3.1 | 647 | 4 | US-09-702-953B-2 | |
| 319 | 6 | 3.1 | 540 | 4 | US-09-212-168-3 | Sequence 3, Appli | 392 | 6 | 3.1 | | | | |

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|-----|---|-----|-----|---|----------------------|-------------------|-----|---|-----|------|---|----------------------|-------------------|
| 393 | 6 | 3.1 | 659 | 1 | US-08-240-049B-16 | Sequence 16, Appl | 466 | 6 | 3.1 | 893 | 4 | US-09-019-160-6 | Sequence 6, Appli |
| 394 | 6 | 3.1 | 659 | 1 | US-08-259-148A-20 | Sequence 20, Appl | 467 | 6 | 3.1 | 893 | 4 | US-09-019-160-7 | Sequence 7, Appli |
| 395 | 6 | 3.1 | 659 | 1 | US-08-484-054-20 | Sequence 20, Appl | 468 | 6 | 3.1 | 893 | 4 | US-09-019-160-8 | Sequence 8, Appli |
| 396 | 6 | 3.1 | 659 | 2 | US-07-876-941A-20 | Sequence 20, Appl | 469 | 6 | 3.1 | 893 | 4 | US-09-019-160-9 | Sequence 9, Appli |
| 397 | 6 | 3.1 | 659 | 3 | US-08-477-292-14 | Sequence 14, Appl | 470 | 6 | 3.1 | 893 | 4 | US-09-238-471-3 | Sequence 3, Appli |
| 398 | 6 | 3.1 | 659 | 4 | US-07-870-985A-20 | Sequence 20, Appl | 471 | 6 | 3.1 | 893 | 5 | PCT-US96-08641-2 | Sequence 4186, Ap |
| 399 | 6 | 3.1 | 659 | 4 | US-08-240-049B-15 | Sequence 15, Appl | 472 | 6 | 3.1 | 893 | 4 | US-09-543-681A-4186 | Sequence 2, Appli |
| 400 | 6 | 3.1 | 660 | 1 | US-08-259-148A-19 | Sequence 19, Appl | 473 | 6 | 3.1 | 912 | 5 | PCT-US95-03747-2 | Sequence 5208, Ap |
| 401 | 6 | 3.1 | 660 | 1 | US-08-484-054-19 | Sequence 19, Appl | 474 | 6 | 3.1 | 914 | 4 | US-09-134-001C-5208 | Sequence 4, Appli |
| 402 | 6 | 3.1 | 660 | 2 | US-07-876-941A-19 | Sequence 19, Appl | 475 | 6 | 3.1 | 947 | 2 | US-08-500-857A-4 | Sequence 4167, Ap |
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| 404 | 6 | 3.1 | 660 | 3 | US-08-478-507-8 | Sequence 8, Appli | 477 | 6 | 3.1 | 992 | 4 | US-09-252-931A-27095 | Sequence 10, Appl |
| 405 | 6 | 3.1 | 660 | 3 | US-08-809-523-2 | Sequence 2, Appli | 478 | 6 | 3.1 | 1048 | 4 | US-09-171-699-10 | Sequence 14, Appl |
| 406 | 6 | 3.1 | 660 | 3 | US-08-542-634-13 | Sequence 13, Appl | 479 | 6 | 3.1 | 1051 | 4 | US-09-428-711A-14 | Sequence 3800, Ap |
| 407 | 6 | 3.1 | 660 | 3 | US-08-542-634-14 | Sequence 14, Appl | 480 | 6 | 3.1 | 1067 | 4 | US-09-134-001C-3800 | Sequence 20, Appl |
| 408 | 6 | 3.1 | 660 | 3 | US-09-128-275A-8 | Sequence 8, Appli | 481 | 6 | 3.1 | 1083 | 4 | US-09-336-643A-20 | Sequence 2, Appli |
| 409 | 6 | 3.1 | 660 | 3 | US-08-471-971-2 | Sequence 13, Appl | 482 | 6 | 3.1 | 1083 | 4 | US-09-600-776-2 | Sequence 1, Appli |
| 410 | 6 | 3.1 | 660 | 3 | US-08-477-292-13 | Sequence 8, Appli | 483 | 6 | 3.1 | 1083 | 4 | US-09-343-494-1 | Sequence 2, Appli |
| 411 | 6 | 3.1 | 660 | 4 | US-09-553-427-8 | Sequence 12, Appl | 484 | 6 | 3.1 | 1083 | 4 | US-09-358-83C-2 | Sequence 3, Appli |
| 412 | 6 | 3.1 | 660 | 4 | US-09-462-606-12 | Sequence 12, Appl | 485 | 6 | 3.1 | 1122 | 2 | US-08-619-198-3 | Sequence 225, App |
| 413 | 6 | 3.1 | 660 | 4 | US-09-462-606-48 | Sequence 48, Appl | 486 | 6 | 3.1 | 1132 | 3 | US-08-851-843A-225 | Sequence 2, Appli |
| 414 | 6 | 3.1 | 660 | 4 | US-09-462-606-49 | Sequence 49, Appl | 487 | 6 | 3.1 | 1132 | 3 | US-08-974-549A-2 | Sequence 344, App |
| 415 | 6 | 3.1 | 660 | 4 | US-09-462-606-50 | Sequence 50, Appl | 488 | 6 | 3.1 | 1132 | 3 | US-08-974-549A-344 | Sequence 225, App |
| 416 | 6 | 3.1 | 660 | 4 | US-09-462-606-52 | Sequence 52, Appl | 489 | 6 | 3.1 | 1132 | 3 | US-08-854-050-225 | Sequence 225, App |
| 417 | 6 | 3.1 | 660 | 4 | US-09-462-606-53 | Sequence 53, Appl | 490 | 6 | 3.1 | 1132 | 4 | US-09-430-323-225 | Sequence 2, Appli |
| 418 | 6 | 3.1 | 660 | 4 | US-09-462-606-54 | Sequence 54, Appl | 491 | 6 | 3.1 | 1132 | 4 | US-09-128-354-2 | Sequence 2, Appli |
| 419 | 6 | 3.1 | 660 | 4 | US-09-462-606-55 | Sequence 55, Appl | 492 | 6 | 3.1 | 1132 | 4 | US-09-675-321-2 | Sequence 2, Appli |
| 420 | 6 | 3.1 | 660 | 4 | US-09-462-606-56 | Sequence 56, Appl | 493 | 6 | 3.1 | 1132 | 4 | US-09-052-919-2 | Sequence 2, Appli |
| 421 | 6 | 3.1 | 660 | 4 | US-09-462-606-57 | Sequence 57, Appl | 494 | 6 | 3.1 | 1132 | 4 | US-08-912-951-2 | Sequence 2, Appli |
| 422 | 6 | 3.1 | 660 | 4 | US-07-870-985A-19 | Sequence 19, Appl | 495 | 6 | 3.1 | 1132 | 4 | US-09-402-181B-2 | Sequence 344, App |
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| 424 | 6 | 3.1 | 660 | 4 | US-09-472-699-2 | Sequence 2, Appli | 497 | 6 | 3.1 | 1132 | 4 | US-09-721-456-2 | Sequence 344, App |
| 425 | 6 | 3.1 | 660 | 5 | PCT-US93-08849A-2 | Sequence 2, Appli | 498 | 6 | 3.1 | 1132 | 4 | US-09-721-456-344 | Sequence 2, Appli |
| 426 | 6 | 3.1 | 660 | 5 | PCT-US93-08849-2 | Sequence 2, Appli | 499 | 6 | 3.1 | 1132 | 4 | US-09-953-052-2 | Sequence 611, App |
| 427 | 6 | 3.1 | 660 | 5 | PCT-US95-13703-13 | Sequence 13, Appl | 500 | 6 | 3.1 | 1154 | 3 | US-08-974-549A-611 | Sequence 323, App |
| 428 | 6 | 3.1 | 660 | 5 | PCT-US95-13703-14 | Sequence 14, Appl | 501 | 6 | 3.1 | 1154 | 4 | US-08-912-951-323 | Sequence 611, App |
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| 432 | 6 | 3.1 | 703 | 4 | US-09-252-991A-26000 | Sequence 26000, A | 505 | 6 | 3.1 | 1189 | 3 | US-08-974-549A-613 | Sequence 613, App |
| 433 | 6 | 3.1 | 708 | 4 | US-09-019-160-5 | Sequence 5, Appli | 506 | 6 | 3.1 | 1189 | 4 | US-08-912-951-325 | Sequence 325, App |
| 434 | 6 | 3.1 | 713 | 3 | US-09-335-409-11 | Sequence 11, Appl | 507 | 6 | 3.1 | 1189 | 4 | US-09-402-181B-613 | Sequence 613, App |
| 435 | 6 | 3.1 | 713 | 4 | US-09-558-102-11 | Sequence 11, Appl | 508 | 6 | 3.1 | 1189 | 4 | US-09-721-456-613 | Sequence 613, App |
| 436 | 6 | 3.1 | 713 | 4 | US-09-567-969-11 | Sequence 11, Appl | 509 | 6 | 3.1 | 1200 | 3 | US-08-974-549A-612 | Sequence 612, App |
| 437 | 6 | 3.1 | 713 | 4 | US-09-568-480-11 | Sequence 11, Appl | 510 | 6 | 3.1 | 1200 | 4 | US-08-912-951-324 | Sequence 324, App |
| 438 | 6 | 3.1 | 713 | 4 | US-09-568-486-11 | Sequence 11, Appl | 511 | 6 | 3.1 | 1200 | 4 | US-09-402-181B-612 | Sequence 612, App |
| 439 | 6 | 3.1 | 713 | 4 | US-09-568-472-11 | Sequence 11, Appl | 512 | 6 | 3.1 | 1200 | 4 | US-09-721-456-612 | Sequence 3, Appli |
| 440 | 6 | 3.1 | 716 | 4 | US-09-816-093-4 | Sequence 11, Appl | 513 | 6 | 3.1 | 1257 | 3 | US-09-220-641-3 | Sequence 600, App |
| 441 | 6 | 3.1 | 735 | 4 | US-09-636-791A-13 | Sequence 13, Appl | 514 | 6 | 3.1 | 1285 | 3 | US-08-974-549A-600 | Sequence 314, App |
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| 443 | 6 | 3.1 | 754 | 2 | US-08-941-262-3 | Sequence 3, Appli | 516 | 6 | 3.1 | 1285 | 4 | US-09-402-181B-600 | Sequence 600, App |
| 444 | 6 | 3.1 | 755 | 2 | US-08-941-262-3 | Sequence 3, Appli | 517 | 6 | 3.1 | 1285 | 4 | US-09-721-456-600 | Sequence 628, App |
| 445 | 6 | 3.1 | 760 | 4 | US-09-252-991A-31724 | Sequence 31724, A | 518 | 6 | 3.1 | 1389 | 2 | US-08-619-198-5 | Sequence 334, App |
| 446 | 6 | 3.1 | 773 | 4 | US-09-889-914B-2 | Sequence 2, Appli | 519 | 6 | 3.1 | 1407 | 3 | US-08-974-549A-628 | Sequence 628, App |
| 447 | 6 | 3.1 | 776 | 4 | US-09-523-849-34 | Sequence 34, Appl | 520 | 6 | 3.1 | 1407 | 4 | US-08-912-951-334 | Sequence 334, App |
| 448 | 6 | 3.1 | 794 | 1 | US-08-188-228-60 | Sequence 60, Appl | 521 | 6 | 3.1 | 1407 | 4 | US-09-402-181B-628 | Sequence 628, App |
| 449 | 6 | 3.1 | 794 | 1 | US-08-332-643-54 | Sequence 54, Appl | 522 | 6 | 3.1 | 1407 | 4 | US-09-402-181B-628 | Sequence 628, App |
| 450 | 6 | 3.1 | 794 | 1 | US-08-332-643-54 | Sequence 54, Appl | 523 | 6 | 3.1 | 1416 | 1 | US-08-061-465-4 | Sequence 4, Appli |
| 451 | 6 | 3.1 | 794 | 1 | US-08-332-643-54 | Sequence 54, Appl | 524 | 6 | 3.1 | 1436 | 2 | US-08-652-971-2 | Sequence 2, Appli |
| 452 | 6 | 3.1 | 807 | 3 | US-08-974-549A-5 | Sequence 5, Appli | 525 | 6 | 3.1 | 1436 | 2 | US-08-991-258A-2 | Sequence 2, Appli |
| 453 | 6 | 3.1 | 807 | 4 | US-08-912-951-5 | Sequence 5, Appli | 526 | 6 | 3.1 | 1436 | 2 | US-08-769-399-2 | Sequence 2, Appli |
| 454 | 6 | 3.1 | 807 | 4 | US-09-402-181B-5 | Sequence 5, Appli | 527 | 6 | 3.1 | 1436 | 2 | US-08-991-953A-2 | Sequence 2, Appli |
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| 456 | 6 | 3.1 | 816 | 4 | US-09-252-991A-28790 | Sequence 28790, A | 529 | 6 | 3.1 | 1525 | 3 | US-09-540-245A-2 | Sequence 2, Appli |
| 457 | 6 | 3.1 | 845 | 4 | US-09-641-741-29 | Sequence 29, Appl | 530 | 6 | 3.1 | 1525 | 3 | US-09-540-153-2 | Sequence 2, Appli |
| 458 | 6 | 3.1 | 851 | 4 | US-09-252-991A-16684 | Sequence 16684, A | 531 | 6 | 3.1 | 1528 | 1 | US-08-463-092B-6 | Sequence 6, Appli |
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| 460 | 6 | 3.1 | 867 | 4 | US-09-417-485D-4 | Sequence 4, Appli | 533 | 6 | 3.1 | 1528 | 2 | US-08-460-907B-6 | Sequence 6, Appli |
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| 462 | 6 | 3.1 | 893 | 2 | US-08-706-702-3 | Sequence 3, Appli | 535 | 6 | 3.1 | 1528 | 3 | US-08-461-384B-6 | Sequence 396, App |
| 463 | 6 | 3.1 | 893 | 3 | US-08-484-661A-2 | Sequence 2, Appli | 536 | 6 | 3.1 | 1529 | 4 | US-09-312-283C-396 | Sequence 72, Appl |
| 464 | 6 | 3.1 | 893 | 3 | US-08-706-706-3 | Sequence 3, Appli | 537 | 6 | 3.1 | 1622 | 4 | US-09-231-899-72 | Sequence 8, Appli |
| 465 | 6 | 3.1 | 893 | 4 | US-08-656-664-2 | Sequence 2, Appli | 538 | 6 | 3.1 | 1786 | 3 | US-08-973-462-8 | |

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| 539 | 6 | 3.1 | 2125 | 4 | US-09-919-172-29 | Sequence 29, Appl | 612 | 5 | 2.6 | 19 | 4 | US-09-626-580C-57 | Sequence 57, Appl |
| 540 | 6 | 3.1 | 2172 | 1 | US-08-611-107-31 | Sequence 31, Appl | 613 | 5 | 2.6 | 19 | 4 | US-09-749-959-49 | Sequence 49, Appl |
| 541 | 6 | 3.1 | 2257 | 1 | US-08-611-107-10 | Sequence 10, Appl | 614 | 5 | 2.6 | 20 | 3 | US-09-162-934-13 | Sequence 13, Appl |
| 542 | 6 | 3.1 | 2257 | 3 | US-08-422-560A-10 | Sequence 10, Appl | 615 | 5 | 2.6 | 20 | 4 | US-09-769-180-26 | Sequence 26, Appl |
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| 751 | 5 | 2.6 | 38 | 4 | US-09-010-317-37 | Sequence 37, Appl | 824 | 5 | 2.6 | 55 | 4 | US-09-621-976-6682 | Sequence 74, Appl |
| 752 | 5 | 2.6 | 38 | 4 | US-09-010-317-37 | Sequence 37, Appl | 825 | 5 | 2.6 | 56 | 4 | US-09-621-976-6682 | Sequence 74, Appl |
| 753 | 5 | 2.6 | 39 | 2 | US-08-488-161-33 | Sequence 33, Appl | 826 | 5 | 2.6 | 57 | 4 | US-09-621-976-6682 | Sequence 74, Appl |
| 754 | 5 | 2.6 | 39 | 2 | US-09-273-685-33 | Sequence 33, Appl | 827 | 5 | 2.6 | 58 | 3 | US-09-621-976-6682 | Sequence 74, Appl |
| 755 | 5 | 2.6 | 39 | 3 | US-09-082-279B-1059 | Sequence 1059, App | 828 | 5 | 2.6 | 58 | 4 | US-09-621-976-6682 | Sequence 74, Appl |
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| 757 | 5 | 2.6 | 39 | 4 | US-09-315-304B-1059 | Sequence 1059, App | 830 | 5 | 2.6 | 59 | 3 | US-09-621-976-6682 | Sequence 74, Appl |

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| 831 | 5 | 2.6 | 59 | 4 | US-09-229-911A-38 | Sequence 38, Appl | 904 | 5 | 2.6 | 78 | 2 | US-07-885-089B-32 | Sequence 32, Appl |
| 832 | 5 | 2.6 | 59 | 4 | US-09-621-976-7401 | Sequence 7401, Ap | 905 | 5 | 2.6 | 78 | 4 | US-09-149-476-356 | Sequence 356, App |
| 833 | 5 | 2.6 | 60 | 1 | US-08-471-780C-87 | Sequence 87, Appl | 906 | 5 | 2.6 | 78 | 4 | US-08-828-683A-23 | Sequence 23, Appl |
| 834 | 5 | 2.6 | 60 | 1 | US-08-467-282B-87 | Sequence 87, Appl | 907 | 5 | 2.6 | 79 | 2 | US-07-885-089B-33 | Sequence 33, Appl |
| 835 | 5 | 2.6 | 60 | 2 | US-08-471-282A-87 | Sequence 87, Appl | 908 | 5 | 2.6 | 79 | 4 | US-09-134-001C-3727 | Sequence 3727, Ap |
| 836 | 5 | 2.6 | 60 | 2 | US-08-466-710C-87 | Sequence 87, Appl | 909 | 5 | 2.6 | 79 | 4 | US-09-186-002-4 | Sequence 4, Appli |
| 837 | 5 | 2.6 | 60 | 3 | US-08-468-739C-87 | Sequence 87, Appl | 910 | 5 | 2.6 | 79 | 4 | US-09-377-468B-26 | Sequence 26, Appl |
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| 839 | 5 | 2.6 | 60 | 4 | US-09-621-976-6003 | Sequence 6003, Ap | 912 | 5 | 2.6 | 79 | 4 | US-09-247-155-93 | Sequence 93, Appl |
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| 841 | 5 | 2.6 | 61 | 4 | US-09-328-352-7170 | Sequence 7170, Ap | 914 | 5 | 2.6 | 80 | 4 | US-09-107-532A-5588 | Sequence 5588, Ap |
| 842 | 5 | 2.6 | 61 | 6 | US-09-621-976-4504 | Sequence 4504, Ap | 915 | 5 | 2.6 | 80 | 4 | US-09-489-039A-13031 | Sequence 13031, A |
| 843 | 5 | 2.6 | 61 | 6 | 5164304-13 | Patent No. 5164304 | 916 | 5 | 2.6 | 81 | 4 | US-09-564-805-211 | Sequence 211, App |
| 844 | 5 | 2.6 | 63 | 4 | US-09-621-976-5530 | Sequence 5530, Ap | 917 | 5 | 2.6 | 81 | 4 | US-09-107-532A-4732 | Sequence 4732, Ap |
| 845 | 5 | 2.6 | 63 | 6 | 5182210-14 | Sequence 5530, Ap | 918 | 5 | 2.6 | 81 | 4 | US-09-543-681A-5027 | Sequence 5027, Ap |
| 846 | 5 | 2.6 | 63 | 6 | 5198542-11 | Patent No. 5198542 | 919 | 5 | 2.6 | 81 | 4 | US-09-543-681A-5027 | Sequence 5027, Ap |
| 847 | 5 | 2.6 | 64 | 4 | US-08-894-626-3 | Sequence 3, Appli | 920 | 5 | 2.6 | 82 | 3 | US-09-084-303B-159 | Sequence 159, App |
| 848 | 5 | 2.6 | 64 | 4 | US-09-489-039A-10494 | Sequence 10494, A | 921 | 5 | 2.6 | 82 | 3 | US-08-483-577A-160 | Sequence 160, App |
| 849 | 5 | 2.6 | 64 | 4 | US-09-621-976-6883 | Sequence 6883, Ap | 922 | 5 | 2.6 | 82 | 3 | US-08-897-438-160 | Sequence 160, App |
| 850 | 5 | 2.6 | 65 | 1 | US-08-435-040-2 | Sequence 2, Appli | 923 | 5 | 2.6 | 82 | 3 | US-08-897-438-160 | Sequence 160, App |
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| 852 | 5 | 2.6 | 65 | 3 | US-09-328-352-5255 | Sequence 5255, Ap | 925 | 5 | 2.6 | 82 | 3 | US-08-897-438-160 | Sequence 160, App |
| 853 | 5 | 2.6 | 65 | 3 | US-08-569-147-85 | Sequence 85, Appl | 926 | 5 | 2.6 | 82 | 3 | US-08-897-438-160 | Sequence 160, App |
| 854 | 5 | 2.6 | 66 | 4 | US-09-257-179-113 | Sequence 85, Appl | 927 | 5 | 2.6 | 83 | 2 | US-08-897-438-160 | Sequence 160, App |
| 855 | 5 | 2.6 | 66 | 4 | US-09-107-532A-6100 | Sequence 6100, Ap | 928 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
| 856 | 5 | 2.6 | 67 | 1 | US-08-471-780C-126 | Sequence 126, App | 929 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
| 857 | 5 | 2.6 | 67 | 1 | US-08-467-282B-126 | Sequence 126, App | 930 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
| 858 | 5 | 2.6 | 67 | 2 | US-08-471-282A-126 | Sequence 126, App | 931 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
| 859 | 5 | 2.6 | 67 | 2 | US-08-466-710C-126 | Sequence 126, App | 932 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
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| 861 | 5 | 2.6 | 67 | 4 | US-09-252-991A-22054 | Sequence 22054, A | 934 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
| 862 | 5 | 2.6 | 67 | 4 | US-09-543-681A-7835 | Sequence 7835, Ap | 935 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
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| 865 | 5 | 2.6 | 68 | 4 | US-09-527-236A-23 | Sequence 23, Appl | 938 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
| 866 | 5 | 2.6 | 68 | 4 | US-09-328-352-7550 | Sequence 7550, Ap | 939 | 5 | 2.6 | 83 | 2 | US-07-885-089B-18 | Sequence 18, Appl |
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| 868 | 5 | 2.6 | 68 | 4 | US-09-756-854-23 | Sequence 23, Appl | 941 | 5 | 2.6 | 84 | 4 | US-09-069-827A-120 | Sequence 120, App |
| 869 | 5 | 2.6 | 70 | 3 | US-08-911-321-7 | Sequence 7, Appli | 942 | 5 | 2.6 | 84 | 4 | US-09-069-827A-120 | Sequence 120, App |
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| 873 | 5 | 2.6 | 70 | 4 | US-09-732-210-1105 | Sequence 1105, Ap | 946 | 5 | 2.6 | 85 | 4 | US-09-732-210-1104 | Sequence 1104, Ap |
| 874 | 5 | 2.6 | 70 | 4 | US-09-489-039A-14233 | Sequence 14233, A | 947 | 5 | 2.6 | 85 | 4 | US-09-732-210-1104 | Sequence 1104, Ap |
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| 877 | 5 | 2.6 | 71 | 4 | US-09-023-151-23 | Sequence 23, Appl | 950 | 5 | 2.6 | 85 | 4 | US-09-621-976-5507 | Sequence 5007, Ap |
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| 886 | 5 | 2.6 | 72 | 4 | US-09-621-976-7585 | Sequence 7585, Ap | 959 | 5 | 2.6 | 85 | 4 | US-09-621-976-5507 | Sequence 5007, Ap |
| 887 | 5 | 2.6 | 72 | 4 | US-09-621-976-7585 | Sequence 7585, Ap | 960 | 5 | 2.6 | 85 | 4 | US-09-621-976-5507 | Sequence 5007, Ap |
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| 890 | 5 | 2.6 | 72 | 4 | US-09-621-976-7585 | Sequence 7585, Ap | 963 | 5 | 2.6 | 85 | 4 | US-09-621-976-5507 | Sequence 5007, Ap |
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| 902 | 5 | 2.6 | 72 | 4 | US-09-621-976-7585 | Sequence 7585, Ap | 975 | 5 | 2.6 | 85 | 4 | US-09-621-976-5507 | Sequence 5007, Ap |
| 903 | 5 | 2.6 | 72 | 2 | US-07-885-089B-30 | Sequence 30, Appl | 976 | 5 | 2.6 | 85 | 4 | US-09-621-976-5507 | Sequence 5007, Ap |

us-10-621-401-145.oligo.rai

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Sequence 11, Appl
Sequence 7121, Ap
Sequence 31, Appl
Sequence 25156, A
Sequence 12, Appl
Sequence 106, App
Sequence 11, Appl
Sequence 381, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 381, App
Sequence 40, Appl
Sequence 1175, Ap
Sequence 3, Appl
Sequence 9, Appl
Sequence 15, Appl
Sequence 2, Appl
Sequence 23, Appl
Sequence 2, Appl
Sequence 13, Appl
Sequence 18, Appl
Sequence 4212, Ap
Sequence 4, Appl
Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-155-171B-16
; Sequence 16, Application US/08155171B
; Patent No. 5543264
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Mangel, Walter F.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/851,217
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/545,585
FILING DATE: 29-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
US-08-155-171B-16

Query Match 4.1%; Score 8; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GCGSYFLG 94
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Db 16 GCGSYFLG 23
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RESULT 2
US-08-435-998-16
; Sequence 16, Application US/08435998
; Patent No. 5935840
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Mangel, Walter F.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,998
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,171
FILING DATE: 19-NOV-1993
APPLICATION NUMBER: US 07/851,217
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/545,585
FILING DATE: 29-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-435-998-16

Query Match 4.1%; Score 8; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GCGSYFLG 94
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Db 16 GCGSYFLG 23
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RESULT 3
US-08-038-343A-5
; Sequence 5, Application US/08038343A

Patent No. 5427928
GENERAL INFORMATION:
APPLICANT: Slesarev, Alexei I
TITLE OF INVENTION: Thermostable Prokaryotic DNA
TITLE OF INVENTION: Topoisomerase V
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,343A
FILING DATE: 24-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9727
TELEPHONE: (310) 445-1140
TELEFAX: (310) 445-9031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Methanopyrus kandleri
US-08-038-343A-5

Query Match 3.6%; Score 7; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194
Db 10 EEEKEEL 16

RESULT 4
US-08-185-414E-4
Sequence 4, Application US/08185414E
Patent No. 5556953
GENERAL INFORMATION:
APPLICANT: Zhang, Lei
APPLICANT: Vijay, Hari M.
TITLE OF INVENTION: ALLERGEN OF CLADOSPORIUM HERBARUM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,414E

FILING DATE: January 24, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1747
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: yeast ribosomal P2 protein
LOCATION: 1...106
US-08-185-414E-4

Query Match 3.6%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 AEEKEE 193
Db 84 AEEKEE 90

RESULT 5
US-09-250-609-2
Sequence 2, Application US/09250609A
Patent No. 6458943
GENERAL INFORMATION:
APPLICANT: Byrne, Jennifer A.
TITLE OF INVENTION: Members of the D52 Gene Family
FILE REFERENCE: 1383.0210002
CURRENT APPLICATION NUMBER: US/09/250,609A
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-09-250-609-2

Query Match 3.6%; Score 7; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 EEEKEEL 194
Db 46 EEEKEEL 52

RESULT 6
US-09-250-611-2
Sequence 2, Application US/09250611
Patent No. 6528283
GENERAL INFORMATION:
APPLICANT: Byrne, Jennifer A.
APPLICANT: Basset, Paul
TITLE OF INVENTION: Members of the D52 Gene Family
FILE REFERENCE: 1383.0210001
CURRENT APPLICATION NUMBER: US/09/250,611
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 144
TYPE: PRT

us-10-621-401-145.oligo.ra1

Mon May 17 11:51:01 2004

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; ORGANISM: Homo sapiens
US-09-250-611-2
Query Match 3.6%; Score 7; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194
DB 46 EEEKEEL 52

RESULT 7
US-09-216-393B-73
; Sequence 73, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 73
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-73

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Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 RSLGFVS 152
DB 62 RSLGFVS 68

RESULT 8
US-09-134-000C-3705
; Sequence 3705, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3705
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3705

Query Match 3.6%; Score 7; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 ESMDLGI 105
DB 72 ESMDLGI 78

RESULT 9
US-08-715-204-1
; Sequence 1, Application US/08715204
; Patent No. 5874286
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer.
; APPLICANT: Zweiger, Gary B.
; TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,204
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0126 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-715-204-1

Query Match 3.6%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194
DB 33 EEEKEEL 39

RESULT 10
US-08-691-814B-10
; Sequence 10, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC

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Mon May 17 11:51:01 2004

COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-691-814B-10

Query Match 3.6%; Score 7; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 32;
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QY 188 EEEKEEL 194
Db 33 EEEKEEL 39
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; Sequence 1, Application US/09162597
; Patent No. 6043343
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer.
; APPLICANT: Zweiger, Gary B.
; TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,597
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/715,204
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0126 US
TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 597-1
US-09-162-597-1

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; Sequence 4, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-250-609-4

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Best Local Similarity 100.0%; Pred. No. 32;
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RESULT 13
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; Sequence 9, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.0
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; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-250-609-9

Query Match 3.6%; Score 7; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 EEEKEEL 194

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RESULT 14
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; Sequence 4, Application US/09250611
; Patent No. 6528283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Bassett, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-250-611-4

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Qy      |||||
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Db      |||||
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; Sequence 9, Application US/09250611
; Patent No. 6528283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Bassett, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-250-611-9

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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188 EEEKEEL 194

Db      |||||
33 EEEKEEL 39

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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US-10-621-401-145

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 193 | 99.5 | 195 | 10 | US-09-305-736-144 |
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| 14 | 7 | 3.6 | 87 | 9 | US-09-764-860-494 |
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| 20 | 3.6 | 112 | 10 | US-09-847-208-62 | Sequence 62, Appl |
| 21 | 3.6 | 124 | 14 | US-10-156-761-8204 | Sequence 8204, Ap |
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| 23 | 3.6 | 176 | 14 | US-10-321-856-73 | Sequence 73, Appl |
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| 27 | 3.6 | 204 | 9 | US-09-250-611-4 | Sequence 4, Appli |
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| 40 | 3.6 | 327 | 12 | US-10-282-122A-66710 | Sequence 66710, A |
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| 42 | 3.6 | 327 | 12 | US-10-072-012-342 | Sequence 342, App |
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| 44 | 3.6 | 366 | 9 | US-09-765-272-16 | Sequence 16, Appl |
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| 104 | 6 | 3.1 | 36 | 9 | US-09-925-300-1022 | Sequence 1022, App | 177 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 105 | 6 | 3.1 | 41 | 9 | US-09-864-761-42758 | Sequence 18, Appl | 178 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 106 | 6 | 3.1 | 41 | 14 | US-09-975-374A-18 | Sequence 228, App | 179 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 107 | 6 | 3.1 | 41 | 15 | US-10-144-929-228 | Sequence 228, App | 180 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 108 | 6 | 3.1 | 41 | 15 | US-10-144-929-228 | Sequence 228, App | 181 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 109 | 6 | 3.1 | 44 | 10 | US-09-764-891-3534 | Sequence 3534, App | 182 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 110 | 6 | 3.1 | 46 | 9 | US-09-738-626-4422 | Sequence 4422, App | 183 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 111 | 6 | 3.1 | 46 | 15 | US-10-375-932-130 | Sequence 130, App | 184 | 78 | 9 | US-09-989-729-363 | Sequence 363, App |
| 112 | 6 | 3.1 | 46 | 15 | US-10-375-932-131 | Sequence 131, App | 185 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 113 | 6 | 3.1 | 46 | 15 | US-10-375-932-131 | Sequence 131, App | 186 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 114 | 6 | 3.1 | 47 | 12 | US-10-424-599-202959 | Sequence 202959, A | 187 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 115 | 6 | 3.1 | 47 | 12 | US-10-424-599-266223 | Sequence 266223, A | 188 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 116 | 6 | 3.1 | 48 | 14 | US-10-424-599-26493 | Sequence 26493, A | 189 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 117 | 6 | 3.1 | 51 | 11 | US-09-864-408A-4080 | Sequence 4080, App | 190 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 118 | 6 | 3.1 | 51 | 12 | US-10-424-599-150848 | Sequence 150848, A | 191 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 119 | 6 | 3.1 | 52 | 9 | US-09-864-761-43582 | Sequence 43582, A | 192 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 120 | 6 | 3.1 | 52 | 9 | US-09-864-761-47325 | Sequence 47325, A | 193 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 121 | 6 | 3.1 | 52 | 12 | US-10-424-599-177066 | Sequence 177066, A | 194 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 122 | 6 | 3.1 | 52 | 12 | US-10-425-114-71273 | Sequence 71273, A | 195 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 123 | 6 | 3.1 | 54 | 9 | US-09-864-761-39215 | Sequence 39215, A | 196 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 124 | 6 | 3.1 | 54 | 9 | US-09-864-761-44300 | Sequence 44300, A | 197 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 125 | 6 | 3.1 | 54 | 9 | US-09-864-761-44300 | Sequence 44300, A | 198 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 126 | 6 | 3.1 | 54 | 13 | US-10-424-599-274266 | Sequence 274266, A | 199 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 127 | 6 | 3.1 | 54 | 13 | US-10-016-157A-193 | Sequence 193, App | 200 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 128 | 6 | 3.1 | 54 | 14 | US-10-219-329-7 | Sequence 7, Appl | 201 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 129 | 6 | 3.1 | 54 | 14 | US-10-153-185-7 | Sequence 7, Appl | 202 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 130 | 6 | 3.1 | 54 | 14 | US-10-153-185-7 | Sequence 7, Appl | 203 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 131 | 6 | 3.1 | 55 | 9 | US-09-764-855-138 | Sequence 138, App | 204 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 132 | 6 | 3.1 | 55 | 12 | US-10-424-599-169367 | Sequence 169367, A | 205 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 133 | 6 | 3.1 | 55 | 12 | US-10-424-599-284170 | Sequence 284170, A | 206 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 134 | 6 | 3.1 | 55 | 14 | US-10-072-349-138 | Sequence 138, App | 207 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 135 | 6 | 3.1 | 56 | 9 | US-09-864-761-47236 | Sequence 47236, A | 208 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 136 | 6 | 3.1 | 56 | 12 | US-10-424-599-200649 | Sequence 200649, A | 209 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 137 | 6 | 3.1 | 59 | 12 | US-10-424-599-146489 | Sequence 146489, A | 210 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
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| 139 | 6 | 3.1 | 62 | 12 | US-10-282-122A-49293 | Sequence 49293, A | 212 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 140 | 6 | 3.1 | 62 | 12 | US-10-424-599-163598 | Sequence 163598, A | 213 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
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| 142 | 6 | 3.1 | 64 | 9 | US-09-864-761-45501 | Sequence 45501, A | 215 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 143 | 6 | 3.1 | 64 | 12 | US-10-424-599-242476 | Sequence 242476, A | 216 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 144 | 6 | 3.1 | 67 | 14 | US-10-106-698-5627 | Sequence 5627, App | 217 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 145 | 6 | 3.1 | 68 | 12 | US-10-424-599-153256 | Sequence 153256, A | 218 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 146 | 6 | 3.1 | 68 | 12 | US-10-424-599-245964 | Sequence 245964, A | 219 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 147 | 6 | 3.1 | 70 | 10 | US-09-813-153-100 | Sequence 100, App | 220 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 148 | 6 | 3.1 | 71 | 12 | US-10-424-599-181953 | Sequence 181953, A | 221 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 149 | 6 | 3.1 | 71 | 12 | US-10-424-599-225874 | Sequence 225874, A | 222 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 150 | 6 | 3.1 | 72 | 12 | US-10-424-599-180657 | Sequence 180657, A | 223 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 151 | 6 | 3.1 | 73 | 12 | US-10-424-599-242233 | Sequence 242233, A | 224 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
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| 153 | 6 | 3.1 | 74 | 9 | US-09-925-302-509 | Sequence 509, App | 226 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 154 | 6 | 3.1 | 74 | 9 | US-09-864-761-35685 | Sequence 35685, A | 227 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
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| 156 | 6 | 3.1 | 75 | 9 | US-09-864-761-40141 | Sequence 40141, A | 229 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 157 | 6 | 3.1 | 75 | 15 | US-10-264-049-3362 | Sequence 3362, App | 230 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
| 158 | 6 | 3.1 | 76 | 12 | US-10-424-599-153444 | Sequence 153444, A | 231 | 78 | 10 | US-09-989-729-363 | Sequence 363, App |
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| 236 | 6 | 3.1 | 78 | 12 | US-10-063-745-363 | Sequence 66, Appl | 309 | 6 | 3.1 | 78 | 14 | US-10-063-502-66 | Sequence 66, Appl |
| 237 | 6 | 3.1 | 78 | 12 | US-09-989-724-363 | Sequence 363, App | 310 | 6 | 3.1 | 78 | 14 | US-10-173-700-242 | Sequence 242, App |
| 238 | 6 | 3.1 | 78 | 12 | US-09-989-728-363 | Sequence 363, App | 311 | 6 | 3.1 | 78 | 14 | US-10-174-572-242 | Sequence 242, App |
| 239 | 6 | 3.1 | 78 | 12 | US-09-990-441-363 | Sequence 363, App | 312 | 6 | 3.1 | 78 | 14 | US-10-174-579-242 | Sequence 242, App |
| 240 | 6 | 3.1 | 78 | 12 | US-10-063-512-66 | Sequence 66, Appl | 313 | 6 | 3.1 | 78 | 14 | US-10-174-582-242 | Sequence 242, App |
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| 247 | 6 | 3.1 | 78 | 12 | US-10-176-483-242 | Sequence 242, App | 320 | 6 | 3.1 | 78 | 14 | US-10-176-747-242 | Sequence 242, App |
| 248 | 6 | 3.1 | 78 | 12 | US-10-176-749-242 | Sequence 242, App | 321 | 6 | 3.1 | 78 | 14 | US-10-176-750-242 | Sequence 242, App |
| 249 | 6 | 3.1 | 78 | 12 | US-10-176-914-242 | Sequence 242, App | 322 | 6 | 3.1 | 78 | 14 | US-10-176-985-242 | Sequence 242, App |
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| 251 | 6 | 3.1 | 78 | 12 | US-09-997-857-363 | Sequence 363, App | 324 | 6 | 3.1 | 78 | 14 | US-10-176-992-242 | Sequence 242, App |
| 252 | 6 | 3.1 | 78 | 12 | US-10-063-555-66 | Sequence 66, Appl | 325 | 6 | 3.1 | 78 | 14 | US-10-176-993-242 | Sequence 242, App |
| 253 | 6 | 3.1 | 78 | 12 | US-10-063-563-66 | Sequence 66, Appl | 326 | 6 | 3.1 | 78 | 14 | US-10-184-658-242 | Sequence 242, App |
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| 258 | 6 | 3.1 | 78 | 12 | US-10-180-550-242 | Sequence 242, App | 331 | 6 | 3.1 | 78 | 14 | US-10-174-576-242 | Sequence 242, App |
| 259 | 6 | 3.1 | 78 | 12 | US-10-183-014-242 | Sequence 242, App | 332 | 6 | 3.1 | 78 | 14 | US-10-174-585-242 | Sequence 242, App |
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| 261 | 6 | 3.1 | 78 | 12 | US-10-187-740-242 | Sequence 242, App | 334 | 6 | 3.1 | 78 | 14 | US-10-175-747-242 | Sequence 242, App |
| 262 | 6 | 3.1 | 78 | 12 | US-10-187-883-242 | Sequence 242, App | 335 | 6 | 3.1 | 78 | 14 | US-10-176-481-242 | Sequence 242, App |
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| 265 | 6 | 3.1 | 78 | 12 | US-10-194-463-242 | Sequence 242, App | 338 | 6 | 3.1 | 78 | 14 | US-10-176-493-242 | Sequence 242, App |
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| 267 | 6 | 3.1 | 78 | 12 | US-10-195-884-242 | Sequence 242, App | 340 | 6 | 3.1 | 78 | 14 | US-10-176-911-242 | Sequence 242, App |
| 268 | 6 | 3.1 | 78 | 12 | US-10-195-896-242 | Sequence 242, App | 341 | 6 | 3.1 | 78 | 14 | US-10-176-919-242 | Sequence 242, App |
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| 271 | 6 | 3.1 | 78 | 12 | US-10-196-757-242 | Sequence 242, App | 344 | 6 | 3.1 | 78 | 14 | US-10-179-510-242 | Sequence 242, App |
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| 276 | 6 | 3.1 | 78 | 12 | US-10-199-304-242 | Sequence 242, App | 349 | 6 | 3.1 | 78 | 14 | US-10-180-549-242 | Sequence 242, App |
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| 278 | 6 | 3.1 | 78 | 12 | US-10-199-313-242 | Sequence 242, App | 351 | 6 | 3.1 | 78 | 14 | US-10-180-559-242 | Sequence 242, App |
| 279 | 6 | 3.1 | 78 | 12 | US-10-199-456-242 | Sequence 242, App | 352 | 6 | 3.1 | 78 | 14 | US-10-181-000-242 | Sequence 242, App |
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| 285 | 6 | 3.1 | 78 | 12 | US-10-206-928-242 | Sequence 242, App | 358 | 6 | 3.1 | 78 | 14 | US-10-184-646-242 | Sequence 242, App |
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| 288 | 6 | 3.1 | 78 | 12 | US-10-207-922-242 | Sequence 242, App | 361 | 6 | 3.1 | 78 | 14 | US-10-187-594-242 | Sequence 242, App |
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| 291 | 6 | 3.1 | 78 | 12 | US-09-991-150-363 | Sequence 363, App | 364 | 6 | 3.1 | 78 | 14 | US-10-187-885-242 | Sequence 242, App |
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| 294 | 6 | 3.1 | 78 | 12 | US-10-066-867-66 | Sequence 66, Appl | 367 | 6 | 3.1 | 78 | 14 | US-10-176-760-242 | Sequence 242, App |
| 295 | 6 | 3.1 | 78 | 12 | US-10-052-586-242 | Sequence 242, App | 368 | 6 | 3.1 | 78 | 14 | US-10-176-990-242 | Sequence 242, App |
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| 299 | 6 | 3.1 | 78 | 12 | US-10-175-737-242 | Sequence 242, App | 372 | 6 | 3.1 | 78 | 14 | US-10-180-551-242 | Sequence 242, App |
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| 305 | 6 | 3.1 | 78 | 12 | US-10-176-757-242 | Sequence 242, App | 378 | 6 | 3.1 | 78 | 14 | US-10-184-616-242 | Sequence 242, App |
| 306 | 6 | 3.1 | 78 | 12 | US-10-176-913-242 | Sequence 242, App | 379 | 6 | 3.1 | 78 | 14 | US-10-184-616-242 | Sequence 242, App |
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| 393 | 6 | 3.1 | 78 | 14 | US-10-187-597-242 | Sequence 242, App | 466 |
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| 396 | 6 | 3.1 | 78 | 14 | US-10-187-602-242 | Sequence 242, App | 469 |
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| 410 | 6 | 3.1 | 78 | 14 | US-10-188-770-242 | Sequence 242, App | 483 |
| 411 | 6 | 3.1 | 78 | 14 | US-10-188-773-242 | Sequence 242, App | 484 |
| 412 | 6 | 3.1 | 78 | 14 | US-10-188-781-242 | Sequence 242, App | 485 |
| 413 | 6 | 3.1 | 78 | 14 | US-10-194-361-242 | Sequence 242, App | 486 |
| 414 | 6 | 3.1 | 78 | 14 | US-10-194-343-242 | Sequence 242, App | 487 |
| 415 | 6 | 3.1 | 78 | 14 | US-10-193-897-242 | Sequence 242, App | 488 |
| 416 | 6 | 3.1 | 78 | 14 | US-10-195-901-242 | Sequence 242, App | 489 |
| 417 | 6 | 3.1 | 78 | 14 | US-10-195-902-242 | Sequence 242, App | 490 |
| 418 | 6 | 3.1 | 78 | 14 | US-10-196-743-242 | Sequence 242, App | 491 |
| 419 | 6 | 3.1 | 78 | 14 | US-10-196-760-242 | Sequence 242, App | 492 |
| 420 | 6 | 3.1 | 78 | 14 | US-10-173-708-242 | Sequence 242, App | 493 |
| 421 | 6 | 3.1 | 78 | 14 | US-10-176-479-242 | Sequence 242, App | 494 |
| 422 | 6 | 3.1 | 78 | 14 | US-10-176-748-242 | Sequence 242, App | 495 |
| 423 | 6 | 3.1 | 78 | 14 | US-10-176-916-242 | Sequence 242, App | 496 |
| 424 | 6 | 3.1 | 78 | 14 | US-10-179-507-242 | Sequence 242, App | 497 |
| 425 | 6 | 3.1 | 78 | 14 | US-10-179-516-242 | Sequence 242, App | 498 |
| 426 | 6 | 3.1 | 78 | 14 | US-10-179-519-242 | Sequence 242, App | 499 |
| 427 | 6 | 3.1 | 78 | 14 | US-10-179-525-242 | Sequence 242, App | 500 |
| 428 | 6 | 3.1 | 78 | 14 | US-10-180-540-242 | Sequence 242, App | 501 |
| 429 | 6 | 3.1 | 78 | 14 | US-10-180-545-242 | Sequence 242, App | 502 |
| 430 | 6 | 3.1 | 78 | 14 | US-10-183-006-242 | Sequence 242, App | 503 |
| 431 | 6 | 3.1 | 78 | 14 | US-10-183-008-242 | Sequence 242, App | 504 |
| 432 | 6 | 3.1 | 78 | 14 | US-10-183-017-242 | Sequence 242, App | 505 |
| 433 | 6 | 3.1 | 78 | 14 | US-10-183-019-242 | Sequence 242, App | 506 |
| 434 | 6 | 3.1 | 78 | 14 | US-10-184-618-242 | Sequence 242, App | 507 |
| 435 | 6 | 3.1 | 78 | 14 | US-10-184-625-242 | Sequence 242, App | 508 |
| 436 | 6 | 3.1 | 78 | 14 | US-10-184-626-242 | Sequence 242, App | 509 |
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| 442 | 6 | 3.1 | 78 | 14 | US-10-188-774-242 | Sequence 242, App | 515 |
| 443 | 6 | 3.1 | 78 | 14 | US-10-188-775-242 | Sequence 242, App | 516 |
| 444 | 6 | 3.1 | 78 | 14 | US-10-194-463-242 | Sequence 242, App | 517 |
| 445 | 6 | 3.1 | 78 | 14 | US-10-196-745-242 | Sequence 242, App | 518 |
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| 449 | 6 | 3.1 | 78 | 14 | US-10-176-484-242 | Sequence 242, App | 522 |
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| 459 | 6 | 3.1 | 78 | 14 | US-10-183-015-242 | Sequence 242, App | 532 |
| 460 | 6 | 3.1 | 78 | 14 | US-10-184-615-242 | Sequence 242, App | 533 |
| 461 | 6 | 3.1 | 78 | 14 | US-10-184-620-242 | Sequence 242, App | 534 |
| 462 | 6 | 3.1 | 78 | 14 | US-10-184-643-242 | Sequence 242, App | 535 |
| 463 | 6 | 3.1 | 78 | 14 | US-10-184-656-242 | Sequence 242, App | 536 |
| 464 | 6 | 3.1 | 78 | 14 | US-10-192-010-242 | Sequence 242, App | 537 |
| 465 | 6 | 3.1 | 78 | 14 | US-10-205-908-242 | Sequence 242, App | 538 |
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| 470 | 6 | 3.1 | 78 | 14 | US-10-187-750-242 | Sequence 242, App | 543 |
| 471 | 6 | 3.1 | 78 | 14 | US-10-188-780-242 | Sequence 242, App | 544 |
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| 473 | 6 | 3.1 | 78 | 14 | US-10-196-748-242 | Sequence 242, App | 546 |
| 474 | 6 | 3.1 | 78 | 14 | US-10-196-750-242 | Sequence 242, App | 547 |
| 475 | 6 | 3.1 | 78 | 14 | US-10-197-659-242 | Sequence 242, App | 548 |
| 476 | 6 | 3.1 | 78 | 14 | US-10-197-705-242 | Sequence 242, App | 549 |
| 477 | 6 | 3.1 | 78 | 14 | US-10-197-705-242 | Sequence 242, App | 550 |
| 478 | 6 | 3.1 | 78 | 14 | US-10-197-708-242 | Sequence 242, App | 551 |
| 479 | 6 | 3.1 | 78 | 14 | US-10-197-708-242 | Sequence 242, App | 552 |
| 480 | 6 | 3.1 | 78 | 14 | US-10-198-764-242 | Sequence 242, App | 553 |
| 481 | 6 | 3.1 | 78 | 14 | US-10-198-765-242 | Sequence 242, App | 554 |
| 482 | 6 | 3.1 | 78 | 14 | US-10-198-768-242 | Sequence 242, App | 555 |
| 483 | 6 | 3.1 | 78 | 14 | US-10-198-769-242 | Sequence 242, App | 556 |
| 484 | 6 | 3.1 | 78 | 14 | US-10-199-305-242 | Sequence 242, App | 557 |
| 485 | 6 | 3.1 | 78 | 14 | US-10-199-306-242 | Sequence 242, App | 558 |
| 486 | 6 | 3.1 | 78 | 14 | US-10-199-310-242 | Sequence 242, App | 559 |
| 487 | 6 | 3.1 | 78 | 14 | US-10-199-311-242 | Sequence 242, App | 560 |
| 488 | 6 | 3.1 | 78 | 14 | US-10-199-311-242 | Sequence 242, App | 561 |
| 489 | 6 | 3.1 | 78 | 14 | US-10-199-314-242 | Sequence 242, App | 562 |
| 490 | 6 | 3.1 | 78 | 14 | US-10-199-317-242 | Sequence 242, App | 563 |
| 491 | 6 | 3.1 | 78 | 14 | US-10-199-665-242 | Sequence 242, App | 564 |
| 492 | 6 | 3.1 | 78 | 14 | US-10-199-666-242 | Sequence 242, App | 565 |
| 493 | 6 | 3.1 | 78 | 14 | US-10-199-669-242 | Sequence 242, App | 566 |
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| 495 | 6 | 3.1 | 78 | 14 | US-10-201-770-242 | Sequence 242, App | 568 |
| 496 | 6 | 3.1 | 78 | 14 | US-10-201-855-242 | Sequence 242, App | 569 |
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| 514 | 6 | 3.1 | 78 | 14 | US-10-227-693-66 | Sequence 66, Appl | 587 |
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| 520 | 6 | 3.1 | 78 | 14 | US-10-194-461-242 | Sequence 242, App | 593 |
| 521 | 6 | 3.1 | 78 | 14 | US-10-195-892-242 | Sequence 242, App | 594 |
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| 526 | 6 | 3.1 | 78 | 14 | US-10-197-707-242 | Sequence 242, App | 599 |
| 527 | 6 | 3.1 | 78 | 14 | US-10-199-303-242 | Sequence 242, App | 600 |

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| 527 | 6 | 3.1 | 78 | 14 | US-10-199-318-242 | Sequence 242, App | 600 | 6 | 3.1 | 78 | 14 | US-10-199-460-242 | Sequence 242, App |
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| 529 | 6 | 3.1 | 78 | 14 | US-10-199-462-242 | Sequence 242, App | 602 | 6 | 3.1 | 78 | 14 | US-10-199-667-242 | Sequence 242, App |
| 530 | 6 | 3.1 | 78 | 14 | US-10-201-324-242 | Sequence 242, App | 603 | 6 | 3.1 | 78 | 14 | US-10-199-673-242 | Sequence 242, App |
| 531 | 6 | 3.1 | 78 | 14 | US-10-201-328-242 | Sequence 242, App | 604 | 6 | 3.1 | 78 | 14 | US-10-201-321-242 | Sequence 242, App |
| 532 | 6 | 3.1 | 78 | 14 | US-10-201-527-242 | Sequence 242, App | 605 | 6 | 3.1 | 78 | 14 | US-10-201-322-242 | Sequence 242, App |
| 533 | 6 | 3.1 | 78 | 14 | US-10-201-528-242 | Sequence 242, App | 606 | 6 | 3.1 | 78 | 14 | US-10-201-326-242 | Sequence 242, App |
| 534 | 6 | 3.1 | 78 | 14 | US-10-201-530-242 | Sequence 242, App | 607 | 6 | 3.1 | 78 | 14 | US-10-201-532-242 | Sequence 242, App |
| 535 | 6 | 3.1 | 78 | 14 | US-10-202-408-242 | Sequence 242, App | 608 | 6 | 3.1 | 78 | 14 | US-10-201-533-242 | Sequence 242, App |
| 536 | 6 | 3.1 | 78 | 14 | US-10-202-409-242 | Sequence 242, App | 609 | 6 | 3.1 | 78 | 14 | US-10-201-535-242 | Sequence 242, App |
| 537 | 6 | 3.1 | 78 | 14 | US-10-202-411-242 | Sequence 242, App | 610 | 6 | 3.1 | 78 | 14 | US-10-201-769-242 | Sequence 242, App |
| 538 | 6 | 3.1 | 78 | 14 | US-10-202-472-242 | Sequence 242, App | 611 | 6 | 3.1 | 78 | 14 | US-10-201-771-242 | Sequence 242, App |
| 539 | 6 | 3.1 | 78 | 14 | US-10-205-502-242 | Sequence 242, App | 612 | 6 | 3.1 | 78 | 14 | US-10-201-854-242 | Sequence 242, App |
| 540 | 6 | 3.1 | 78 | 14 | US-10-205-507-242 | Sequence 242, App | 613 | 6 | 3.1 | 78 | 14 | US-10-202-410-242 | Sequence 242, App |
| 541 | 6 | 3.1 | 78 | 14 | US-10-205-511-242 | Sequence 242, App | 614 | 6 | 3.1 | 78 | 14 | US-10-202-473-242 | Sequence 242, App |
| 542 | 6 | 3.1 | 78 | 14 | US-10-205-902-242 | Sequence 242, App | 615 | 6 | 3.1 | 78 | 14 | US-10-202-474-242 | Sequence 242, App |
| 543 | 6 | 3.1 | 78 | 14 | US-10-205-907-242 | Sequence 242, App | 616 | 6 | 3.1 | 78 | 14 | US-10-205-503-242 | Sequence 242, App |
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| 545 | 6 | 3.1 | 78 | 14 | US-10-194-456-242 | Sequence 242, App | 618 | 6 | 3.1 | 78 | 14 | US-10-205-894-242 | Sequence 242, App |
| 546 | 6 | 3.1 | 78 | 14 | US-10-196-758-242 | Sequence 242, App | 619 | 6 | 3.1 | 78 | 14 | US-10-205-896-242 | Sequence 242, App |
| 547 | 6 | 3.1 | 78 | 14 | US-10-198-770-242 | Sequence 242, App | 620 | 6 | 3.1 | 78 | 14 | US-10-205-898-242 | Sequence 242, App |
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| 549 | 6 | 3.1 | 78 | 14 | US-10-200-617-242 | Sequence 242, App | 622 | 6 | 3.1 | 78 | 14 | US-10-205-903-242 | Sequence 242, App |
| 550 | 6 | 3.1 | 78 | 14 | US-10-205-893-242 | Sequence 242, App | 623 | 6 | 3.1 | 78 | 14 | US-10-206-909-242 | Sequence 242, App |
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| 555 | 6 | 3.1 | 78 | 14 | US-10-176-923-242 | Sequence 242, App | 628 | 6 | 3.1 | 78 | 14 | US-10-206-913-242 | Sequence 242, App |
| 556 | 6 | 3.1 | 78 | 14 | US-10-183-011-242 | Sequence 242, App | 629 | 6 | 3.1 | 78 | 14 | US-10-206-914-242 | Sequence 242, App |
| 557 | 6 | 3.1 | 78 | 14 | US-10-184-633-242 | Sequence 242, App | 630 | 6 | 3.1 | 78 | 14 | US-10-206-920-242 | Sequence 242, App |
| 558 | 6 | 3.1 | 78 | 14 | US-10-184-639-242 | Sequence 242, App | 631 | 6 | 3.1 | 78 | 14 | US-10-206-921-242 | Sequence 242, App |
| 559 | 6 | 3.1 | 78 | 14 | US-10-187-742-242 | Sequence 242, App | 632 | 6 | 3.1 | 78 | 14 | US-10-206-923-242 | Sequence 242, App |
| 560 | 6 | 3.1 | 78 | 14 | US-10-187-748-242 | Sequence 242, App | 633 | 6 | 3.1 | 78 | 14 | US-10-206-925-242 | Sequence 242, App |
| 561 | 6 | 3.1 | 78 | 14 | US-10-188-766-242 | Sequence 242, App | 634 | 6 | 3.1 | 78 | 14 | US-10-206-926-242 | Sequence 242, App |
| 562 | 6 | 3.1 | 78 | 14 | US-10-188-771-242 | Sequence 242, App | 635 | 6 | 3.1 | 78 | 14 | US-10-206-927-242 | Sequence 242, App |
| 563 | 6 | 3.1 | 78 | 14 | US-10-192-008-242 | Sequence 242, App | 636 | 6 | 3.1 | 78 | 14 | US-10-207-916-242 | Sequence 242, App |
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| 565 | 6 | 3.1 | 78 | 14 | US-10-192-014-242 | Sequence 242, App | 638 | 6 | 3.1 | 78 | 14 | US-10-207-918-242 | Sequence 242, App |
| 566 | 6 | 3.1 | 78 | 14 | US-10-192-014-242 | Sequence 242, App | 639 | 6 | 3.1 | 78 | 14 | US-10-207-919-242 | Sequence 242, App |
| 567 | 6 | 3.1 | 78 | 14 | US-10-192-016-242 | Sequence 242, App | 640 | 6 | 3.1 | 78 | 14 | US-10-207-920-242 | Sequence 242, App |
| 568 | 6 | 3.1 | 78 | 14 | US-10-194-362-242 | Sequence 242, App | 641 | 6 | 3.1 | 78 | 14 | US-10-207-925-242 | Sequence 242, App |
| 569 | 6 | 3.1 | 78 | 14 | US-10-194-364-242 | Sequence 242, App | 642 | 6 | 3.1 | 78 | 14 | US-10-208-021-242 | Sequence 242, App |
| 570 | 6 | 3.1 | 78 | 14 | US-10-194-395-242 | Sequence 242, App | 643 | 6 | 3.1 | 78 | 14 | US-10-208-022-242 | Sequence 242, App |
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| 572 | 6 | 3.1 | 78 | 14 | US-10-194-458-242 | Sequence 242, App | 645 | 6 | 3.1 | 78 | 14 | US-10-208-026-242 | Sequence 242, App |
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| 575 | 6 | 3.1 | 78 | 14 | US-10-194-488-242 | Sequence 242, App | 648 | 6 | 3.1 | 78 | 14 | US-10-063-567-66 | Sequence 66, App1 |
| 576 | 6 | 3.1 | 78 | 14 | US-10-195-886-242 | Sequence 242, App | 649 | 6 | 3.1 | 78 | 14 | US-10-232-232-242 | Sequence 242, App |
| 577 | 6 | 3.1 | 78 | 14 | US-10-195-891-242 | Sequence 242, App | 650 | 6 | 3.1 | 78 | 14 | US-10-195-898-242 | Sequence 242, App |
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| 579 | 6 | 3.1 | 78 | 14 | US-10-196-752-242 | Sequence 242, App | 652 | 6 | 3.1 | 78 | 14 | US-10-173-693-242 | Sequence 242, App |
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| 581 | 6 | 3.1 | 78 | 14 | US-10-196-761-242 | Sequence 242, App | 654 | 6 | 3.1 | 78 | 14 | US-10-175-741-242 | Sequence 242, App |
| 582 | 6 | 3.1 | 78 | 14 | US-10-197-692-242 | Sequence 242, App | 655 | 6 | 3.1 | 78 | 14 | US-10-175-750-242 | Sequence 242, App |
| 583 | 6 | 3.1 | 78 | 14 | US-10-197-693-242 | Sequence 242, App | 656 | 6 | 3.1 | 78 | 14 | US-10-176-986-242 | Sequence 242, App |
| 584 | 6 | 3.1 | 78 | 14 | US-10-197-696-242 | Sequence 242, App | 657 | 6 | 3.1 | 78 | 14 | US-10-184-641-242 | Sequence 242, App |
| 585 | 6 | 3.1 | 78 | 14 | US-10-197-703-242 | Sequence 242, App | 658 | 6 | 3.1 | 78 | 14 | US-10-187-888-242 | Sequence 242, App |
| 586 | 6 | 3.1 | 78 | 14 | US-10-198-757-242 | Sequence 242, App | 659 | 6 | 3.1 | 78 | 14 | US-10-194-360-242 | Sequence 242, App |
| 587 | 6 | 3.1 | 78 | 14 | US-10-198-761-242 | Sequence 242, App | 660 | 6 | 3.1 | 78 | 14 | US-10-194-365-242 | Sequence 242, App |
| 588 | 6 | 3.1 | 78 | 14 | US-10-198-762-242 | Sequence 242, App | 661 | 6 | 3.1 | 78 | 14 | US-10-195-895-242 | Sequence 242, App |
| 589 | 6 | 3.1 | 78 | 14 | US-10-198-763-242 | Sequence 242, App | 662 | 6 | 3.1 | 78 | 14 | US-10-199-302-242 | Sequence 242, App |
| 590 | 6 | 3.1 | 78 | 14 | US-10-198-767-242 | Sequence 242, App | 663 | 6 | 3.1 | 78 | 14 | US-10-201-323-242 | Sequence 242, App |
| 591 | 6 | 3.1 | 78 | 14 | US-10-198-767-242 | Sequence 242, App | 664 | 6 | 3.1 | 78 | 14 | US-10-205-510-242 | Sequence 242, App |
| 592 | 6 | 3.1 | 78 | 14 | US-10-199-301-242 | Sequence 242, App | 665 | 6 | 3.1 | 78 | 14 | US-10-205-891-242 | Sequence 242, App |
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| 594 | 6 | 3.1 | 78 | 14 | US-10-199-312-242 | Sequence 242, App | 667 | 6 | 3.1 | 78 | 14 | US-10-207-923-242 | Sequence 242, App |
| 595 | 6 | 3.1 | 78 | 14 | US-10-199-315-242 | Sequence 242, App | 668 | 6 | 3.1 | 78 | 14 | US-10-207-924-242 | Sequence 242, App |
| 596 | 6 | 3.1 | 78 | 14 | US-10-199-316-242 | Sequence 242, App | 669 | 6 | 3.1 | 78 | 14 | US-10-208-028-242 | Sequence 242, App |
| 597 | 6 | 3.1 | 78 | 14 | US-10-199-451-242 | Sequence 242, App | 670 | 6 | 3.1 | 78 | 14 | US-10-063-538-66 | Sequence 66, App1 |
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| 599 | 6 | 3.1 | 78 | 14 | US-10-199-459-242 | Sequence 242, App | 672 | 6 | 3.1 | 78 | 14 | US-10-175-753-242 | Sequence 242, App |

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| 820 | 6 | 3.1 | 78 | 14 | US-10-063-732-66 | Sequence 66, Appl | 893 | 6 | 3.1 | 78 | 15 | US-10-195-893-242 | Sequence 242, App |
| 821 | 6 | 3.1 | 78 | 14 | US-10-063-523-66 | Sequence 66, Appl | 894 | 6 | 3.1 | 78 | 15 | US-10-179-509-242 | Sequence 242, App |
| 822 | 6 | 3.1 | 78 | 14 | US-10-063-527-66 | Sequence 66, Appl | 895 | 6 | 3.1 | 78 | 15 | US-10-194-486-242 | Sequence 242, App |
| 823 | 6 | 3.1 | 78 | 14 | US-10-063-529-66 | Sequence 66, Appl | 896 | 6 | 3.1 | 78 | 15 | US-10-195-900-242 | Sequence 242, App |
| 824 | 6 | 3.1 | 78 | 14 | US-10-063-581-66 | Sequence 66, Appl | 897 | 6 | 3.1 | 78 | 15 | US-10-198-759-242 | Sequence 242, App |
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| 826 | 6 | 3.1 | 78 | 14 | US-10-063-589-66 | Sequence 66, Appl | 899 | 6 | 3.1 | 78 | 15 | US-10-199-463-242 | Sequence 242, App |
| 827 | 6 | 3.1 | 78 | 14 | US-10-063-593-66 | Sequence 66, Appl | 900 | 6 | 3.1 | 78 | 15 | US-10-199-523-242 | Sequence 242, App |
| 828 | 6 | 3.1 | 78 | 14 | US-10-063-596-66 | Sequence 66, Appl | 901 | 6 | 3.1 | 78 | 15 | US-10-202-471-242 | Sequence 242, App |
| 829 | 6 | 3.1 | 78 | 14 | US-10-063-600-66 | Sequence 66, Appl | 902 | 6 | 3.1 | 78 | 15 | US-10-207-915-242 | Sequence 242, App |
| 830 | 6 | 3.1 | 78 | 14 | US-10-063-604-66 | Sequence 66, Appl | 903 | 6 | 3.1 | 78 | 15 | US-10-213-538-363 | Sequence 363, App |
| 831 | 6 | 3.1 | 78 | 14 | US-10-063-607-66 | Sequence 66, Appl | 904 | 6 | 3.1 | 78 | 16 | US-10-197-709-242 | Sequence 242, App |
| 832 | 6 | 3.1 | 78 | 14 | US-10-063-612-66 | Sequence 66, Appl | 905 | 6 | 3.1 | 80 | 9 | US-09-864-761-35659 | Sequence 35659, A |
| 833 | 6 | 3.1 | 78 | 14 | US-10-063-615-66 | Sequence 66, Appl | 906 | 6 | 3.1 | 81 | 12 | US-10-424-599-216251 | Sequence 216251, A |
| 834 | 6 | 3.1 | 78 | 14 | US-10-063-640-66 | Sequence 66, Appl | 907 | 6 | 3.1 | 82 | 12 | US-10-424-599-252118 | Sequence 252118, A |
| 835 | 6 | 3.1 | 78 | 14 | US-10-063-642-66 | Sequence 66, Appl | 908 | 6 | 3.1 | 82 | 12 | US-10-424-599-259594 | Sequence 259594, A |
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| 837 | 6 | 3.1 | 78 | 14 | US-10-063-649-66 | Sequence 66, Appl | 910 | 6 | 3.1 | 85 | 12 | US-10-424-599-190825 | Sequence 190825, A |
| 838 | 6 | 3.1 | 78 | 14 | US-10-063-650-66 | Sequence 66, Appl | 911 | 6 | 3.1 | 86 | 9 | US-09-864-761-39192 | Sequence 39192, A |
| 839 | 6 | 3.1 | 78 | 14 | US-10-063-652-66 | Sequence 66, Appl | 912 | 6 | 3.1 | 86 | 11 | US-09-864-408A-7192 | Sequence 7192, A |
| 840 | 6 | 3.1 | 78 | 14 | US-10-063-654-66 | Sequence 66, Appl | 913 | 6 | 3.1 | 86 | 11 | US-09-833-245-868 | Sequence 868, App |
| 841 | 6 | 3.1 | 78 | 14 | US-10-063-659-66 | Sequence 66, Appl | 914 | 6 | 3.1 | 87 | 9 | US-09-864-761-39625 | Sequence 39625, A |
| 842 | 6 | 3.1 | 78 | 14 | US-10-063-661-66 | Sequence 66, Appl | 915 | 6 | 3.1 | 87 | 9 | US-09-864-761-45003 | Sequence 45003, A |
| 843 | 6 | 3.1 | 78 | 14 | US-10-063-540-66 | Sequence 66, Appl | 916 | 6 | 3.1 | 87 | 12 | US-10-351-334-326 | Sequence 326, App |
| 844 | 6 | 3.1 | 78 | 14 | US-10-063-540-66 | Sequence 66, Appl | 917 | 6 | 3.1 | 88 | 12 | US-10-424-599-179331 | Sequence 179331, A |
| 845 | 6 | 3.1 | 78 | 14 | US-10-063-568-66 | Sequence 66, Appl | 918 | 6 | 3.1 | 89 | 12 | US-09-864-761-44120 | Sequence 44120, A |
| 846 | 6 | 3.1 | 78 | 14 | US-10-063-570-66 | Sequence 66, Appl | 919 | 6 | 3.1 | 89 | 12 | US-09-764-856-49 | Sequence 49, Appl |
| 847 | 6 | 3.1 | 78 | 14 | US-10-063-582-66 | Sequence 66, Appl | 920 | 6 | 3.1 | 91 | 9 | US-10-102-627-49 | Sequence 49, Appl |
| 848 | 6 | 3.1 | 78 | 14 | US-10-063-587-66 | Sequence 66, Appl | 921 | 6 | 3.1 | 91 | 9 | US-09-864-761-34175 | Sequence 34175, A |
| 849 | 6 | 3.1 | 78 | 14 | US-10-063-592-66 | Sequence 66, Appl | 922 | 6 | 3.1 | 92 | 9 | US-09-893-737-204 | Sequence 204, App |
| 850 | 6 | 3.1 | 78 | 14 | US-10-063-597-66 | Sequence 66, Appl | 923 | 6 | 3.1 | 92 | 14 | US-10-137-765-51 | Sequence 51, Appl |
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| 852 | 6 | 3.1 | 78 | 14 | US-10-063-606-66 | Sequence 66, Appl | 925 | 6 | 3.1 | 93 | 12 | US-10-424-599-146730 | Sequence 146730, A |
| 853 | 6 | 3.1 | 78 | 14 | US-10-063-609-66 | Sequence 66, Appl | 926 | 6 | 3.1 | 93 | 12 | US-10-424-599-273539 | Sequence 273539, A |
| 854 | 6 | 3.1 | 78 | 14 | US-10-063-611-66 | Sequence 66, Appl | 927 | 6 | 3.1 | 96 | 14 | US-10-156-761-8079 | Sequence 8079, App |
| 855 | 6 | 3.1 | 78 | 14 | US-10-063-614-66 | Sequence 66, Appl | 928 | 6 | 3.1 | 97 | 12 | US-10-424-599-223887 | Sequence 223887, A |
| 856 | 6 | 3.1 | 78 | 14 | US-10-063-639-66 | Sequence 66, Appl | 929 | 6 | 3.1 | 97 | 12 | US-10-425-114-56699 | Sequence 56699, A |
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| 858 | 6 | 3.1 | 78 | 14 | US-10-063-646-66 | Sequence 66, Appl | 931 | 6 | 3.1 | 97 | 14 | US-10-102-806-604 | Sequence 604, App |
| 859 | 6 | 3.1 | 78 | 14 | US-10-063-651-66 | Sequence 66, Appl | 932 | 6 | 3.1 | 97 | 15 | US-10-264-049-2757 | Sequence 2757, App |
| 860 | 6 | 3.1 | 78 | 14 | US-10-063-653-66 | Sequence 66, Appl | 933 | 6 | 3.1 | 98 | 9 | US-09-205-658-58 | Sequence 58, Appl |
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| 862 | 6 | 3.1 | 78 | 14 | US-10-063-665-66 | Sequence 66, Appl | 935 | 6 | 3.1 | 98 | 9 | US-09-864-761-40415 | Sequence 40415, A |
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| 865 | 6 | 3.1 | 78 | 14 | US-10-063-562-66 | Sequence 66, Appl | 938 | 6 | 3.1 | 98 | 12 | US-10-425-114-52612 | Sequence 52612, A |
| 866 | 6 | 3.1 | 78 | 14 | US-10-063-638-66 | Sequence 66, Appl | 939 | 6 | 3.1 | 99 | 9 | US-09-864-761-38013 | Sequence 38013, A |
| 867 | 6 | 3.1 | 78 | 14 | US-10-063-638-66 | Sequence 66, Appl | 940 | 6 | 3.1 | 99 | 9 | US-09-864-761-42990 | Sequence 42990, A |
| 868 | 6 | 3.1 | 78 | 14 | US-10-063-672-66 | Sequence 66, Appl | 941 | 6 | 3.1 | 99 | 14 | US-10-029-386-27410 | Sequence 27410, A |
| 869 | 6 | 3.1 | 78 | 14 | US-10-063-682-66 | Sequence 66, Appl | 942 | 6 | 3.1 | 100 | 12 | US-10-425-114-62186 | Sequence 62186, A |
| 870 | 6 | 3.1 | 78 | 14 | US-10-063-721-66 | Sequence 66, Appl | 943 | 6 | 3.1 | 101 | 12 | US-10-276-774-1655 | Sequence 1655, App |
| 871 | 6 | 3.1 | 78 | 14 | US-10-063-723-66 | Sequence 66, Appl | 944 | 6 | 3.1 | 102 | 12 | US-10-424-599-247392 | Sequence 247392, A |
| 872 | 6 | 3.1 | 78 | 14 | US-10-063-514-66 | Sequence 66, Appl | 945 | 6 | 3.1 | 103 | 12 | US-10-424-599-242138 | Sequence 242138, A |
| 873 | 6 | 3.1 | 78 | 14 | US-10-063-516-66 | Sequence 66, Appl | 946 | 6 | 3.1 | 103 | 12 | US-10-369-493-23002 | Sequence 23002, A |
| 874 | 6 | 3.1 | 78 | 14 | US-10-063-529-66 | Sequence 66, Appl | 947 | 6 | 3.1 | 104 | 12 | US-10-335-977-5013 | Sequence 5013, App |
| 875 | 6 | 3.1 | 78 | 14 | US-10-063-584-66 | Sequence 66, Appl | 948 | 6 | 3.1 | 105 | 12 | US-10-424-599-232000 | Sequence 232000, A |
| 876 | 6 | 3.1 | 78 | 14 | US-10-063-688-66 | Sequence 66, Appl | 949 | 6 | 3.1 | 105 | 14 | US-10-029-386-30635 | Sequence 30635, A |
| 877 | 6 | 3.1 | 78 | 14 | US-10-063-520-66 | Sequence 66, Appl | 950 | 6 | 3.1 | 106 | 9 | US-09-739-438-6 | Sequence 6, Appl |
| 878 | 6 | 3.1 | 78 | 14 | US-10-063-647-66 | Sequence 66, Appl | 951 | 6 | 3.1 | 106 | 12 | US-10-424-599-206052 | Sequence 206052, A |
| 879 | 6 | 3.1 | 78 | 14 | US-10-063-548-66 | Sequence 66, Appl | 952 | 6 | 3.1 | 106 | 12 | US-10-104-047-3270 | Sequence 3270, App |
| 880 | 6 | 3.1 | 78 | 14 | US-10-063-578-66 | Sequence 66, Appl | 953 | 6 | 3.1 | 107 | 12 | US-10-424-599-211471 | Sequence 211471, A |
| 881 | 6 | 3.1 | 78 | 14 | US-10-063-648-66 | Sequence 66, Appl | 954 | 6 | 3.1 | 107 | 15 | US-10-630-590-150 | Sequence 150, App |
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| 883 | 6 | 3.1 | 78 | 14 | US-10-063-718-66 | Sequence 66, Appl | 956 | 6 | 3.1 | 110 | 10 | US-09-847-208-12 | Sequence 12, Appl |
| 884 | 6 | 3.1 | 78 | 14 | US-10-063-741-66 | Sequence 66, Appl | 957 | 6 | 3.1 | 110 | 12 | US-10-282-1228-69197 | Sequence 69197, A |
| 885 | 6 | 3.1 | 78 | 14 | US-10-063-617-66 | Sequence 66, Appl | 958 | 6 | 3.1 | 111 | 10 | US-09-847-208-60 | Sequence 60, Appl |
| 886 | 6 | 3.1 | 78 | 14 | US-10-063-664-66 | Sequence 66, Appl | 959 | 6 | 3.1 | 111 | 12 | US-10-282-1228-55306 | Sequence 55306, A |
| 887 | 6 | 3.1 | 78 | 14 | US-10-063-561-66 | Sequence 66, Appl | 960 | 6 | 3.1 | 111 | 12 | US-10-424-599-181954 | Sequence 181954, A |
| 888 | 6 | 3.1 | 78 | 14 | US-10-063-618-66 | Sequence 66, Appl | 961 | 6 | 3.1 | 111 | 14 | US-10-230-331-30 | Sequence 30, Appl |
| 889 | 6 | 3.1 | 78 | 14 | US-10-063-657-66 | Sequence 66, Appl | 962 | 6 | 3.1 | 113 | 10 | US-09-847-208-9 | Sequence 9, Appl |
| 890 | 6 | 3.1 | 78 | 14 | US-10-063-668-66 | Sequence 66, Appl | 963 | 6 | 3.1 | 113 | 12 | US-10-424-599-244539 | Sequence 244539, A |
| 891 | 6 | 3.1 | 78 | 15 | US-10-063-550-66 | Sequence 66, Appl | 964 | 6 | 3.1 | 113 | 14 | US-10-230-331-31 | Sequence 31, Appl |

PRIOR APPLICATION NUMBER: US 60/064,900
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,988
PRIOR FILING DATE: 1997-11-07
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 611
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 145
LENGTH: 194

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-621-401-145

Query Match 99.5%; Score 193; DB 12; Length 194;
Best Local Similarity 100.0%; Pred. No. 2.3e-180;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLASGFLVLMISLGGGLAQSDTSPDTEESYSDWGLRHLRGSGFESVNSYFDSFLELLGKK 60
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DB 121 TCGANKYRCDAKFRWCLXISCSDLKSLGFSVSKVEACDSLVDVTFTVNTLTCRPFMNSQ 180

QY 181 RAACICAEKEEEL 194
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RESULT 3

US-09-305-736-144
Sequence 144, Application US/09305736
Publication No. US20030088078A1
GENERAL INFORMATION:

APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P1
CURRENT APPLICATION NUMBER: US/09/305,736
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: PCT/US98/23435
EARLIER FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/064,911
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,912
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,983
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,900
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,988
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EARLIER APPLICATION NUMBER: 60/064,987
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,908
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,984
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,985
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,100
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,089

EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,095
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,090
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 612
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 144
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (195)
OTHER INFORMATION: Xaa equals stop translation
US-09-305-736-144

Query Match 99.5%; Score 193; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.3e-180;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 RAACICAEKEEEL 194

RESULT 4

US-09-818-683-144
Sequence 144, Application US/09818683
Publication No. US20030211472A1
GENERAL INFORMATION:

APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P1
CURRENT APPLICATION NUMBER: US/09/818,683
CURRENT FILING DATE: 2001-03-28
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 612
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 144
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (195)
OTHER INFORMATION: Xaa equals stop translation
US-09-818-683-144

Query Match 99.5%; Score 193; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.3e-180;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon May 17 11:51:01 2004

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Y 61 NGVCQYRCRYGKAPMPRGYPKQPNCGSGYFLGLKVPESMDLGIIPAMTKCCNQLDVCYD 120
b 61 NGVCQYRCRYGKAPMPRGYPKQPNCGSGYFLGLKVPESMDLGIIPAMTKCCNQLDVCYD 120
Y 121 TCGANKYRCDAKPRWCLXSLCSDLKSLGSLGFVSKVEACDLSLVDVTFTWTLGCRPFMNSQ 180
b 121 TCGANKYRCDAKPRWCLXSLCSDLKSLGSLGFVSKVEACDLSLVDVTFTWTLGCRPFMNSQ 180
Y 181 RAACICAEKEEL 194
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RESULT 5
US-10-363-616-357
; Sequence 357, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Kysaq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 357
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-357

Query Match 70.6%; Score 137; DB 12; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLASGFLVLSLGGGLAQSPTPTESYSWGLRHLRGSPESVNSYFDSFLELLGGK 60
QY 61 NGVCQYRCRYGKAPMPRGYPKQPNCGSGYFLGLKVPESMDLGIIPAMTKCCNQLDVCYD 120
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QY 121 TCGANKYRCDAKPRWCL 137
Db 121 TCGANKYRCDAKPRWCL 137

RESULT 6
US-09-975-374A-13
; Sequence 13, Application US/09975374A
; Patent No. US20020119139A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: CLONING AND RECOMBINANT EXPRESSION OF MAMMALIAN GROUP
; FILE REFERENCE: 1479-R-00
; CURRENT APPLICATION NUMBER: US/09/975,374A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/239,489
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 194
; TYPE: PRT

; ORGANISM: Xenopus sp.
US-09-975-374A-13
Query Match 4.1%; Score 8; DB 9; Length 194;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 SQAACIC 186
Db 179 SQAACIC 186

RESULT 7
US-10-425-114-45178
; Sequence 45178, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45178
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700455612_FLI.pap
US-10-425-114-45178

Query Match 4.1%; Score 8; DB 12; Length 306;
Best Local Similarity 100.0%; Pred. No. 23;
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QY 187 ABEKEEL 194
Db 227 ABEKEEL 234

RESULT 8
US-10-156-761-13394
; Sequence 13394, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13394
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13394

us-10-621-401-145.oligo.rapb

Mon May 17 11:51:01 2004

Query Match 4.1%; Score 8; DB 14; Length 484;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SGGGLAQ 20
 DB 105 SGGGLAQ 112

RESULT 9
 US-10-425-114-51651
 ; Sequence 51651, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 51651
 ; LENGTH: 679
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700083042_FLI.pep
 US-10-425-114-51651

Query Match 4.1%; Score 8; DB 12; Length 679;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEEL 194
 DB 600 ABEKEEL 607

RESULT 10
 US-10-425-114-56183
 ; Sequence 56183, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 56183
 ; LENGTH: 780
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700210018_FLI.pep
 US-10-425-114-56183

Query Match 4.1%; Score 8; DB 12; Length 780;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEEL 194

Db 701 ABEKEEL 708

RESULT 11
 US-09-774-639-334
 ; Sequence 334, Application US/09774639
 ; Publication No. US20030003555A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 90 Human Secreted Proteins
 ; FILE REFERENCE: PZ013P1
 ; CURRENT APPLICATION NUMBER: US/09/774,639
 ; CURRENT FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
 ; NUMBER OF SEQ ID NOS: 371
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 334
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-774-639-334

Query Match 3.6%; Score 7; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LWSLGG 16
 DB 2 LWSLGG 8

RESULT 12
 US-09-969-730-324
 ; Sequence 324, Application US/09969730
 ; Publication No. US20030054443A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 90 Human Secreted Proteins
 ; FILE REFERENCE: PZ013P2
 ; CURRENT APPLICATION NUMBER: US/09/969,730
 ; CURRENT FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: 09/774,639
 ; PRIOR FILING DATE: 2001-02-01
 ; PRIOR APPLICATION NUMBER: 60/238,291
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 09/244,112
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: PCT/US98/16235
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/056,371
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,732
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,366
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,364
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,370
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,367
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,365
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,731
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,557
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/056,563
 ; PRIOR FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 60/055,970
 ; PRIOR FILING DATE: 1997-08-18

Mon May 17 11:51:01 2004

Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-363-324

Query Match 3.6%; Score 7; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LWSLGG 16
| | | | |
Db 2 LWSLGG 8
| | | | |

RESULT 14
US-09-764-860-494
; Sequence 494, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 494
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-860-494

Query Match 3.6%; Score 7; DB 9; Length 87;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVLWLSL 14
| | | | |
Db 42 LVLWLSL 49
| | | | |

RESULT 15

US-10-424-599-228701
; Sequence 228701, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 228701
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48544C.1.pep
US-10-424-599-228701

Query Match 3.6%; Score 7; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 60/055,986
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,311
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,808
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,803
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,809
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,806
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,310
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,798
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,309
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,312
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,807
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,386
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,373
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-324

Query Match 3.6%; Score 7; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LWSLGG 16
| | | | |
Db 2 LWSLGG 8
| | | | |

RESULT 13

US-10-621-363-324
; Sequence 324, Application US/10621363
; Publication No. US20040023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P20132C1
; CURRENT APPLICATION NUMBER: US/10/621,363
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19

us-10-621-401-145.oligo.rapb

Mon May 17 11:51:01 2004

QY 47 NSYFDSF 53
| | | | |
Db 51 NSYFDSF 57

Search completed: May 17, 2004, 10:58:50
Job time : 80 secs

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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:48:45 ; Search time 20 Seconds
(without alignments)
933.058 Million cell updates/sec

Title: US-10-621-401-145
Perfect score: 194
Sequence: 1 MKLASGLVWLGLGGLAQ.....PFMNSQRAACICAEERKEEL 194

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR.78.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1 | 8 | 4.1 | 214 | 1 | W2AD41 | late I3 23K protei |
| 2 | 8 | 4.1 | 528 | 2 | B96545 | hypothetical prote |
| 3 | 8 | 4.1 | 637 | 2 | T39291 | hypothetical C2H2 |
| 4 | 8 | 4.1 | 768 | 2 | C96545 | hypothetical prote |
| 5 | 7 | 3.6 | 63 | 2 | A12413 | hypothetical prote |
| 6 | 7 | 3.6 | 75 | 2 | C90225 | hypothetical prote |
| 7 | 7 | 3.6 | 75 | 2 | C90342 | hypothetical prote |
| 8 | 7 | 3.6 | 106 | 1 | R5BY1B | acidic ribosomal p |
| 9 | 7 | 3.6 | 106 | 1 | R5BY2B | acidic ribosomal p |
| 10 | 7 | 3.6 | 106 | 2 | T52147 | ribosomal protein |
| 11 | 7 | 3.6 | 110 | 1 | R5BYA1 | acidic ribosomal p |
| 12 | 7 | 3.6 | 111 | 2 | S43115 | acidic ribosomal p |
| 13 | 7 | 3.6 | 191 | 2 | T01132 | cyclin-dependent k |
| 14 | 7 | 3.6 | 255 | 2 | S34144 | lipase - Serratia |
| 15 | 7 | 3.6 | 298 | 2 | T29685 | hypothetical prote |
| 16 | 7 | 3.6 | 317 | 2 | A97684 | hypothetical prote |
| 17 | 7 | 3.6 | 317 | 2 | AB2909 | rhizobiocin (impor |
| 18 | 7 | 3.6 | 319 | 2 | S32923 | phospholipase A1 (|
| 19 | 7 | 3.6 | 320 | 2 | AB0330 | phospholipase A (i |
| 20 | 7 | 3.6 | 327 | 2 | G83058 | probable permease |
| 21 | 7 | 3.6 | 343 | 2 | E64363 | acidic ribosomal p |
| 22 | 7 | 3.6 | 418 | 2 | T01021 | hypothetical prote |
| 23 | 7 | 3.6 | 419 | 2 | G95221 | sugar ABC transpor |
| 24 | 7 | 3.6 | 419 | 2 | F98085 | hypothetical prote |
| 25 | 7 | 3.6 | 420 | 2 | B42400 | sugar-binding prot |
| 26 | 7 | 3.6 | 448 | 2 | F83724 | Na+-transporting A |
| 27 | 7 | 3.6 | 448 | 2 | A24327 | carboxypeptidase E |
| 28 | 7 | 3.6 | 451 | 2 | G70241 | hypothetical prote |
| 29 | 7 | 3.6 | 464 | 2 | G71082 | probable mannose-1 |

| | | | | | | |
|-----|---|-----|------|---|--------|--------------------|
| 30 | 7 | 3.6 | 465 | 2 | G75104 | mannose-6-phosphat |
| 31 | 7 | 3.6 | 476 | 2 | S12461 | carboxypeptidase E |
| 32 | 7 | 3.6 | 476 | 2 | A40469 | carboxypeptidase E |
| 33 | 7 | 3.6 | 476 | 2 | S09489 | carboxypeptidase E |
| 34 | 7 | 3.6 | 477 | 2 | S16383 | carboxypeptidase E |
| 35 | 7 | 3.6 | 519 | 2 | H96661 | unknown protein, 5 |
| 36 | 7 | 3.6 | 557 | 2 | A70480 | carbamoyl-phosphat |
| 37 | 7 | 3.6 | 585 | 2 | S69216 | sulfur deprivation |
| 38 | 7 | 3.6 | 632 | 2 | F96544 | hypothetical prote |
| 39 | 7 | 3.6 | 652 | 2 | A37000 | leukemia virus rec |
| 40 | 7 | 3.6 | 677 | 2 | F83954 | flagella-associate |
| 41 | 7 | 3.6 | 736 | 2 | T00313 | catalase (EC 1.11. |
| 42 | 7 | 3.6 | 780 | 2 | F96840 | hypothetical prote |
| 43 | 7 | 3.6 | 783 | 2 | B96802 | hypothetical prote |
| 44 | 7 | 3.6 | 791 | 2 | T12455 | hypothetical prote |
| 45 | 7 | 3.6 | 812 | 2 | H96544 | ATP-dependent prot |
| 46 | 7 | 3.6 | 816 | 2 | B86705 | probable beta-gala |
| 47 | 7 | 3.6 | 832 | 2 | E84543 | probable heme util |
| 48 | 7 | 3.6 | 851 | 2 | A83484 | hypothetical prote |
| 49 | 7 | 3.6 | 879 | 2 | B84765 | hypothetical prote |
| 50 | 7 | 3.6 | 900 | 2 | F71426 | protein F32E10.3 (|
| 51 | 7 | 3.6 | 990 | 2 | H88733 | alpha-mannosidase |
| 52 | 7 | 3.6 | 1083 | 1 | S53048 | DNA-directed RNA p |
| 53 | 7 | 3.6 | 1135 | 1 | RNF332 | chromosome-associa |
| 54 | 7 | 3.6 | 1231 | 2 | S70553 | G-protein signalin |
| 55 | 7 | 3.6 | 1387 | 2 | JC5502 | hypothetical prote |
| 56 | 7 | 3.6 | 1548 | 2 | T04456 | hypothetical prote |
| 57 | 7 | 3.6 | 2515 | 2 | S47008 | tenascin-like prot |
| 58 | 7 | 3.6 | 4725 | 1 | A4357 | dynein heavy chain |
| 59 | 6 | 3.1 | 62 | 2 | F86783 | hypothetical prote |
| 60 | 6 | 3.1 | 71 | 2 | T18966 | hypothetical prote |
| 61 | 6 | 3.1 | 79 | 2 | T44223 | hypothetical prote |
| 62 | 6 | 3.1 | 84 | 2 | A12925 | conserved hypothet |
| 63 | 6 | 3.1 | 84 | 2 | E98356 | hypothetical prote |
| 64 | 6 | 3.1 | 89 | 2 | PQ0190 | pyruvate, phosphat |
| 65 | 6 | 3.1 | 90 | 2 | PQ0191 | pyruvate, phosphat |
| 66 | 6 | 3.1 | 96 | 2 | A55278 | homeotic protein H |
| 67 | 6 | 3.1 | 99 | 1 | H69208 | hypothetical prote |
| 68 | 6 | 3.1 | 99 | 2 | A90208 | embryonic abundant |
| 69 | 6 | 3.1 | 102 | 2 | S19225 | hypothetical prote |
| 70 | 6 | 3.1 | 102 | 2 | T50981 | hypothetical prote |
| 71 | 6 | 3.1 | 104 | 2 | D43559 | homeotic protein R |
| 72 | 6 | 3.1 | 107 | 2 | A75031 | isu ribosomal prot |
| 73 | 6 | 3.1 | 110 | 2 | T00142 | hypothetical prote |
| 74 | 6 | 3.1 | 111 | 2 | S41866 | acidic ribosomal p |
| 75 | 6 | 3.1 | 111 | 2 | F71216 | probable ribosomal |
| 76 | 6 | 3.1 | 111 | 2 | B81661 | ribosomal protein |
| 77 | 6 | 3.1 | 113 | 2 | S43109 | acidic ribosomal p |
| 78 | 6 | 3.1 | 114 | 1 | R5KT30 | ribosomal protein |
| 79 | 6 | 3.1 | 119 | 2 | S40137 | T-cell receptor V- |
| 80 | 6 | 3.1 | 119 | 2 | S24490 | Ig heavy chain V r |
| 81 | 6 | 3.1 | 120 | 2 | AE1030 | probable membrane |
| 82 | 6 | 3.1 | 120 | 2 | T02037 | acidic ribosomal p |
| 83 | 6 | 3.1 | 122 | 2 | B70026 | hypothetical prote |
| 84 | 6 | 3.1 | 127 | 2 | F64039 | hypothetical prote |
| 85 | 6 | 3.1 | 128 | 2 | A64335 | conserved hypothet |
| 86 | 6 | 3.1 | 129 | 2 | AE1232 | hypothetical prote |
| 87 | 6 | 3.1 | 130 | 2 | AC1825 | SOS ribosomal prot |
| 88 | 6 | 3.1 | 131 | 2 | C75113 | hypothetical prote |
| 89 | 6 | 3.1 | 136 | 2 | A10124 | probable prelin |
| 90 | 6 | 3.1 | 140 | 2 | I47204 | Ig heavy chain var |
| 91 | 6 | 3.1 | 143 | 2 | G71880 | hypothetical prote |
| 92 | 6 | 3.1 | 144 | 2 | AH2443 | hypothetical prote |
| 93 | 6 | 3.1 | 149 | 2 | AC0375 | probable membrane |
| 94 | 6 | 3.1 | 150 | 2 | AG0564 | probable membrane |
| 95 | 6 | 3.1 | 151 | 2 | G44779 | hypothetical prote |
| 96 | 6 | 3.1 | 151 | 2 | G90697 | hypothetical prote |
| 97 | 6 | 3.1 | 152 | 2 | A85548 | hypothetical prote |
| 98 | 6 | 3.1 | 156 | 2 | T18755 | hypothetical prote |
| 99 | 6 | 3.1 | 156 | 2 | F89418 | protein B0413.7 li |
| 100 | 6 | 3.1 | 162 | 2 | E71131 | hypothetical prote |
| 101 | 6 | 3.1 | 163 | 2 | B48766 | ubiquitin-like pro |
| 102 | 6 | 3.1 | 163 | 2 | A48765 | ubiquitin / riboso |

| | | | | | | | | | | | | | |
|-----|---|-----|-----|---|--------|--------------------|-----|---|-----|-----|---|--------|---------------------|
| 103 | 6 | 3.1 | 167 | 2 | E69768 | hypotheical prote | 176 | 6 | 3.1 | 243 | 2 | T34680 | hypotheical prote |
| 104 | 6 | 3.1 | 170 | 2 | F72115 | hypotheical prote | 177 | 6 | 3.1 | 245 | 2 | D82305 | ubiquinol-cytochro |
| 105 | 6 | 3.1 | 171 | 2 | E07095 | glycine cleavage s | 178 | 6 | 3.1 | 246 | 2 | S58499 | auxin regulated pr |
| 106 | 6 | 3.1 | 173 | 2 | S55668 | hypotheical prote | 179 | 6 | 3.1 | 249 | 2 | D46634 | iron-regulated out |
| 107 | 6 | 3.1 | 173 | 2 | T11831 | NADH2 dehydrogenas | 180 | 6 | 3.1 | 249 | 2 | A97154 | uncharacterized pt |
| 108 | 6 | 3.1 | 175 | 2 | T11151 | NADH2 dehydrogenas | 181 | 6 | 3.1 | 250 | 2 | T20256 | hypotheical prote |
| 109 | 6 | 3.1 | 176 | 2 | G70658 | probable arok prot | 182 | 6 | 3.1 | 250 | 2 | C86338 | protein F5M15.20 [|
| 110 | 6 | 3.1 | 178 | 2 | D71451 | MJ0653 homolog PH0 | 183 | 6 | 3.1 | 253 | 2 | T52380 | zinc finger protei |
| 111 | 6 | 3.1 | 181 | 2 | A28782 | cytochrome-c oxida | 184 | 6 | 3.1 | 254 | 2 | E70438 | type 4 prepillin pe |
| 112 | 6 | 3.1 | 181 | 2 | A11686 | hypotheical prote | 185 | 6 | 3.1 | 254 | 2 | H95070 | hypotheical prote |
| 113 | 6 | 3.1 | 182 | 2 | S03259 | methyl coenzyme M | 186 | 6 | 3.1 | 258 | 2 | A70468 | protein W10D9.2 [i |
| 114 | 6 | 3.1 | 183 | 2 | A93262 | hypotheical prote | 187 | 6 | 3.1 | 258 | 2 | H88130 | flagellar biosynth |
| 115 | 6 | 3.1 | 184 | 2 | UC2429 | activin-A protein | 188 | 6 | 3.1 | 259 | 2 | T49825 | protein F10G7.3 [i |
| 116 | 6 | 3.1 | 184 | 2 | A83316 | hypotheical prote | 190 | 6 | 3.1 | 259 | 2 | T49825 | hypotheical prote |
| 117 | 6 | 3.1 | 185 | 2 | D96572 | protein F12M15.6 [| 191 | 6 | 3.1 | 260 | 2 | E83092 | probable cytochrom |
| 118 | 6 | 3.1 | 185 | 2 | T25098 | hypotheical prote | 192 | 6 | 3.1 | 260 | 2 | G82166 | hypotheical prote |
| 119 | 6 | 3.1 | 186 | 2 | D84673 | probable calcium b | 193 | 6 | 3.1 | 262 | 2 | H64311 | unknown protein en |
| 120 | 6 | 3.1 | 188 | 2 | S75643 | hypotheical prote | 194 | 6 | 3.1 | 262 | 2 | H90871 | hypotheical prote |
| 121 | 6 | 3.1 | 188 | 2 | S18956 | fix23-4 protein - | 196 | 6 | 3.1 | 262 | 2 | B85747 | hydrolase, alpha/b |
| 122 | 6 | 3.1 | 191 | 2 | S17505 | ribonuclease - bal | 197 | 6 | 3.1 | 264 | 2 | F75406 | hypotheical prote |
| 123 | 6 | 3.1 | 191 | 2 | AF1135 | hypotheical prote | 199 | 6 | 3.1 | 265 | 2 | T20667 | hypotheical prote |
| 124 | 6 | 3.1 | 194 | 2 | C70035 | transcription regu | 200 | 6 | 3.1 | 266 | 2 | T39301 | probable o-methyl |
| 125 | 6 | 3.1 | 196 | 2 | C84313 | chemotaxis protei | 201 | 6 | 3.1 | 266 | 2 | A97980 | dihydroorotate oxi |
| 126 | 6 | 3.1 | 197 | 2 | F81934 | probable lipoprote | 202 | 6 | 3.1 | 267 | 2 | H86320 | probable MYB47 tra |
| 127 | 6 | 3.1 | 198 | 2 | C27793 | methyl coenzyme M | 203 | 6 | 3.1 | 269 | 2 | T10253 | membrane protein M |
| 128 | 6 | 3.1 | 199 | 2 | T14468 | pollen coat protei | 204 | 6 | 3.1 | 269 | 2 | B95142 | vick protein (impo |
| 129 | 6 | 3.1 | 200 | 2 | D64405 | methyl coenzyme M | 206 | 6 | 3.1 | 269 | 2 | H98009 | hypotheical prote |
| 130 | 6 | 3.1 | 200 | 2 | F85781 | hypotheical prote | 207 | 6 | 3.1 | 271 | 2 | A96011 | probable cell divi |
| 131 | 6 | 3.1 | 200 | 2 | B90933 | hypotheical prote | 208 | 6 | 3.1 | 271 | 2 | T04666 | hypotheical prote |
| 132 | 6 | 3.1 | 202 | 2 | S14705 | hypotheical prote | 209 | 6 | 3.1 | 271 | 2 | A86874 | conserved hypotet |
| 133 | 6 | 3.1 | 203 | 1 | BVECKV | chalcone isomerase | 210 | 6 | 3.1 | 273 | 2 | AD3445 | H+-transporting tw |
| 134 | 6 | 3.1 | 203 | 2 | C90950 | ruvA protein - Esc | 211 | 6 | 3.1 | 277 | 2 | T10251 | vick protein (impo |
| 135 | 6 | 3.1 | 203 | 2 | G85798 | Holliday junction | 212 | 6 | 3.1 | 279 | 2 | G96508 | probable cell divi |
| 136 | 6 | 3.1 | 203 | 2 | AC0743 | Holliday junction | 213 | 6 | 3.1 | 280 | 2 | T04511 | transcription init |
| 137 | 6 | 3.1 | 204 | 2 | S76108 | hypotheical prote | 214 | 6 | 3.1 | 281 | 2 | H64058 | xyloglucan endo-1, |
| 138 | 6 | 3.1 | 204 | 2 | A10250 | Holliday junction | 215 | 6 | 3.1 | 283 | 2 | T07678 | xyloglucan endo-1, |
| 139 | 6 | 3.1 | 205 | 2 | B95077 | conserved hypotet | 216 | 6 | 3.1 | 284 | 2 | S60166 | transcription init |
| 140 | 6 | 3.1 | 206 | 1 | A55169 | pre-T-cell recepto | 217 | 6 | 3.1 | 284 | 2 | T03794 | genome polyprotein |
| 141 | 6 | 3.1 | 206 | 2 | C29525 | methyl coenzyme M | 218 | 6 | 3.1 | 285 | 2 | S60165 | transcription regu |
| 142 | 6 | 3.1 | 206 | 2 | A75508 | hypotheical prote | 219 | 6 | 3.1 | 285 | 2 | T02641 | probable C2H2-type |
| 143 | 6 | 3.1 | 210 | 2 | D87507 | glutathione S-tran | 220 | 6 | 3.1 | 286 | 2 | G71899 | hypotheical prote |
| 144 | 6 | 3.1 | 211 | 2 | S37792 | hypotheical prote | 221 | 6 | 3.1 | 286 | 2 | T48572 | hypotheical prote |
| 145 | 6 | 3.1 | 211 | 2 | B83493 | hypotheical prote | 222 | 6 | 3.1 | 286 | 2 | G71899 | antigen 5401 - Elm |
| 146 | 6 | 3.1 | 213 | 2 | JO0075 | neuromodulin - gol | 223 | 6 | 3.1 | 287 | 2 | A60543 | major intrinsic pr |
| 147 | 6 | 3.1 | 213 | 2 | B81967 | cadmium resistance | 224 | 6 | 3.1 | 288 | 2 | T09794 | xyloglucan endo-1, |
| 148 | 6 | 3.1 | 214 | 2 | T51657 | myb-related transc | 225 | 6 | 3.1 | 288 | 2 | F71402 | CDP-bequose synth |
| 149 | 6 | 3.1 | 217 | 2 | T00592 | GTP-binding protei | 226 | 6 | 3.1 | 289 | 2 | F47070 | branched-chain ami |
| 150 | 6 | 3.1 | 217 | 2 | JC7997 | nucleolar protein, | 227 | 6 | 3.1 | 289 | 2 | C71701 | hypotheical prote |
| 151 | 6 | 3.1 | 218 | 2 | A75150 | hypotheical prote | 228 | 6 | 3.1 | 290 | 2 | B97774 | hypotheical prote |
| 152 | 6 | 3.1 | 218 | 2 | T47706 | hypotheical prote | 229 | 6 | 3.1 | 290 | 2 | S23544 | chitinase (EC 3.2. |
| 153 | 6 | 3.1 | 219 | 2 | T45047 | hypotheical prote | 230 | 6 | 3.1 | 291 | 2 | S31763 | chitinase (EC 3.2. |
| 154 | 6 | 3.1 | 221 | 2 | S24784 | chalcone isomerase | 231 | 6 | 3.1 | 293 | 2 | D89193 | protein T21C9.1 [i |
| 155 | 6 | 3.1 | 221 | 2 | T47592 | hypotheical prote | 232 | 6 | 3.1 | 293 | 2 | G85083 | hypotheical prote |
| 156 | 6 | 3.1 | 221 | 2 | T12996 | hypotheical prote | 233 | 6 | 3.1 | 293 | 2 | T43930 | hypotheical prote |
| 157 | 6 | 3.1 | 222 | 2 | T52019 | ethylene responsiv | 234 | 6 | 3.1 | 295 | 2 | F52326 | adrenocorticotropi |
| 158 | 6 | 3.1 | 224 | 2 | T44351 | Mg(2+) transport A | 235 | 6 | 3.1 | 296 | 2 | JC4046 | adrenocorticotropi |
| 159 | 6 | 3.1 | 225 | 2 | G70340 | conserved hypotet | 236 | 6 | 3.1 | 296 | 2 | D36788 | hypotheical prote |
| 160 | 6 | 3.1 | 225 | 2 | A95021 | conserved hypotet | 237 | 6 | 3.1 | 297 | 2 | S42767 | adrenocorticotropi |
| 161 | 6 | 3.1 | 225 | 2 | G37892 | neuronal growth-re | 238 | 6 | 3.1 | 297 | 2 | T45849 | gene ACH receptor |
| 162 | 6 | 3.1 | 226 | 2 | A26964 | probable aspartate | 239 | 6 | 3.1 | 297 | 2 | A98294 | hypotheical prote |
| 163 | 6 | 3.1 | 226 | 2 | F71181 | cell division prot | 240 | 6 | 3.1 | 299 | 2 | S12022 | permease [imported |
| 164 | 6 | 3.1 | 226 | 2 | F87449 | CMP-NeuNAC synthet | 241 | 6 | 3.1 | 299 | 2 | UG0178 | extensin - rape |
| 165 | 6 | 3.1 | 228 | 2 | C64114 | hypotheical prote | 242 | 6 | 3.1 | 299 | 2 | S12022 | chitinase (EC 3.2. |
| 166 | 6 | 3.1 | 228 | 2 | D86206 | hypotheical prote | 243 | 6 | 3.1 | 299 | 2 | UG0178 | conserved hypotet |
| 167 | 6 | 3.1 | 229 | 2 | T29203 | aspartate racemase | 244 | 6 | 3.1 | 300 | 2 | B75419 | chitinase (EC 3.2. |
| 168 | 6 | 3.1 | 232 | 2 | B75157 | hypotheical prote | 245 | 6 | 3.1 | 302 | 1 | A45511 | chitinase (EC 3.2. |
| 169 | 6 | 3.1 | 232 | 2 | A69501 | hypotheical prote | 246 | 6 | 3.1 | 303 | 1 | S75983 | hypotheical prote |
| 170 | 6 | 3.1 | 236 | 2 | F75443 | probable hydrolase | 247 | 6 | 3.1 | 303 | 2 | T00479 | probable phosphati |
| 171 | 6 | 3.1 | 238 | 2 | UX0320 | rhodanese-like pro | 248 | 6 | 3.1 | 305 | 2 | F84998 | diaminopimelate ep |
| 172 | 6 | 3.1 | 239 | 2 | S58498 | IAA12 protein - Ar | | | | | | | |
| 173 | 6 | 3.1 | 239 | 2 | G83143 | hypotheical prote | | | | | | | |
| 174 | 6 | 3.1 | 242 | 1 | WJMSX3 | homeotic protein H | | | | | | | |
| 175 | 6 | 3.1 | 243 | 2 | F69725 | tRNA methyltransfe | | | | | | | |

| | | | | | | | | | | | | | |
|-----|---|-----|-----|---|--------|---------------------|-----|---|-----|-----|---|--------|---------------------|
| 249 | 6 | 3.1 | 306 | 1 | H65033 | hypothetical prote | 322 | 6 | 3.1 | 352 | 2 | C97496 | hypothetical prote |
| 250 | 6 | 3.1 | 306 | 2 | C91057 | hypothetical prote | 323 | 6 | 3.1 | 354 | 2 | C90173 | 3-dehydroquinat s |
| 251 | 6 | 3.1 | 306 | 2 | G85901 | hypothetical prote | 324 | 6 | 3.1 | 356 | 2 | A46164 | calnexin - human (|
| 252 | 6 | 3.1 | 310 | 1 | K1BETH | thymidine kinase (| 325 | 6 | 3.1 | 356 | 2 | E84458 | hypothetical prote |
| 253 | 6 | 3.1 | 311 | 2 | T10761 | chitinase (EC 3.2. | 326 | 6 | 3.1 | 358 | 2 | AF1457 | chloromuconate cyc |
| 254 | 6 | 3.1 | 312 | 1 | S22397 | pyruvate synthase | 327 | 6 | 3.1 | 359 | 2 | D96696 | protein FlN21.8 [i |
| 255 | 6 | 3.1 | 312 | 2 | E84268 | hypothetical prote | 328 | 6 | 3.1 | 360 | 2 | S59598 | cysteine proteinas |
| 256 | 6 | 3.1 | 312 | 2 | C71806 | hypothetical prote | 329 | 6 | 3.1 | 360 | 2 | D97501 | porphobilinogen sy |
| 257 | 6 | 3.1 | 312 | 2 | G64712 | toxR-activated gen | 330 | 6 | 3.1 | 361 | 1 | KHHH | aleurain (EC 3.4.2 |
| 258 | 6 | 3.1 | 312 | 2 | E70376 | exopolysphatase | 331 | 6 | 3.1 | 361 | 1 | S75507 | 3-dehydroquinat s |
| 259 | 6 | 3.1 | 313 | 2 | A65140 | gtmKR operon regu | 332 | 6 | 3.1 | 361 | 1 | D69005 | hypothetical prote |
| 260 | 6 | 3.1 | 315 | 2 | T28836 | hypothetical prote | 333 | 6 | 3.1 | 361 | 1 | S68268 | apurinic/apyrimidi |
| 261 | 6 | 3.1 | 315 | 2 | AE0166 | probable virulence | 334 | 6 | 3.1 | 361 | 2 | H85018 | hypothetical prote |
| 262 | 6 | 3.1 | 316 | 2 | F83170 | probable oxidoredu | 335 | 6 | 3.1 | 363 | 2 | B48432 | hypothetical prote |
| 263 | 6 | 3.1 | 316 | 2 | D85088 | nitrilase 1 like p | 336 | 6 | 3.1 | 365 | 2 | D97848 | hypothetical prote |
| 264 | 6 | 3.1 | 318 | 2 | A81217 | conserved hypothet | 337 | 6 | 3.1 | 370 | 2 | S77011 | mercuric resistant |
| 265 | 6 | 3.1 | 318 | 2 | B81794 | conserved hypothet | 338 | 6 | 3.1 | 371 | 2 | T36247 | probable 4-hydroxy |
| 266 | 6 | 3.1 | 320 | 2 | S64088 | probable membrane | 339 | 6 | 3.1 | 371 | 2 | B83781 | two-component sens |
| 267 | 6 | 3.1 | 320 | 2 | F64384 | hypothetical prote | 340 | 6 | 3.1 | 373 | 2 | A80604 | probable oxidoredu |
| 268 | 6 | 3.1 | 320 | 2 | AF2714 | conserved hypothet | 341 | 6 | 3.1 | 374 | 2 | A84783 | hypothetical prote |
| 269 | 6 | 3.1 | 320 | 2 | G86010 | regulator of gluc | 342 | 6 | 3.1 | 375 | 2 | T33439 | hypothetical prote |
| 270 | 6 | 3.1 | 322 | 2 | B96014 | probable sugar upt | 343 | 6 | 3.1 | 376 | 2 | T39454 | hypothetical prote |
| 271 | 6 | 3.1 | 325 | 2 | D87619 | conserved hypothet | 344 | 6 | 3.1 | 380 | 2 | H75159 | 3-isopropylmalate |
| 272 | 6 | 3.1 | 325 | 2 | T18283 | hypothetical prote | 345 | 6 | 3.1 | 380 | 2 | B81832 | probable polyamine |
| 273 | 6 | 3.1 | 326 | 2 | AD2353 | delta-aminolevulin | 346 | 6 | 3.1 | 383 | 2 | E90285 | hypothetical prote |
| 274 | 6 | 3.1 | 327 | 2 | S75506 | porphobilinogen sy | 347 | 6 | 3.1 | 384 | 1 | SUTIKA | endopeptidase K (E |
| 275 | 6 | 3.1 | 330 | 2 | H70480 | porphobilinogen sy | 348 | 6 | 3.1 | 384 | 2 | S29130 | calreticulin (clon |
| 276 | 6 | 3.1 | 330 | 2 | E90578 | 30S ribosomal prot | 349 | 6 | 3.1 | 387 | 2 | T17662 | hypothetical prote |
| 277 | 6 | 3.1 | 331 | 2 | G91164 | regulator of gluc | 350 | 6 | 3.1 | 389 | 2 | D90498 | acyl-CoA dehydroge |
| 278 | 6 | 3.1 | 331 | 2 | E84770 | probable serpin [i | 351 | 6 | 3.1 | 390 | 2 | G69044 | N-acetylornithine |
| 279 | 6 | 3.1 | 334 | 2 | H65028 | probable thioisulfa | 352 | 6 | 3.1 | 390 | 2 | T21367 | hypothetical prote |
| 280 | 6 | 3.1 | 334 | 2 | C91052 | probable thioisulfa | 353 | 6 | 3.1 | 395 | 2 | S25851 | calreticulin precu |
| 281 | 6 | 3.1 | 334 | 2 | G85896 | probable thioisulfa | 354 | 6 | 3.1 | 396 | 2 | H75290 | hypothetical prote |
| 282 | 6 | 3.1 | 334 | 2 | A58195 | Cathepsin L (EC 3. | 355 | 6 | 3.1 | 397 | 2 | A33880 | syndecan 2 - human |
| 283 | 6 | 3.1 | 334 | 2 | D87416 | delta-aminolevulin | 356 | 6 | 3.1 | 397 | 2 | D89768 | hypothetical prote |
| 284 | 6 | 3.1 | 334 | 2 | AE3581 | inositol 2-dehydro | 357 | 6 | 3.1 | 400 | 1 | JQ0756 | nicotinate phospho |
| 285 | 6 | 3.1 | 335 | 2 | C64380 | porphobilinogen sy | 358 | 6 | 3.1 | 400 | 1 | F07075 | nicotinate phospho |
| 286 | 6 | 3.1 | 335 | 2 | A72417 | sugar ABC transpor | 359 | 6 | 3.1 | 400 | 2 | D85619 | probable membrane |
| 287 | 6 | 3.1 | 336 | 2 | D71016 | probable thioisulfa | 360 | 6 | 3.1 | 400 | 2 | T35334 | conserved hypothet |
| 288 | 6 | 3.1 | 336 | 2 | B69542 | hypothetical prote | 361 | 6 | 3.1 | 401 | 2 | D83363 | probable integrase |
| 289 | 6 | 3.1 | 337 | 2 | T24387 | probable cysteine | 362 | 6 | 3.1 | 402 | 2 | T03567 | probable integral |
| 290 | 6 | 3.1 | 337 | 2 | AD2719 | delta-aminolevulin | 363 | 6 | 3.1 | 402 | 2 | H81296 | hypothetical prote |
| 291 | 6 | 3.1 | 337 | 2 | A90846 | Hnr protein [impor | 364 | 6 | 3.1 | 402 | 2 | T51526 | TcAB protein [impo |
| 292 | 6 | 3.1 | 337 | 2 | H85703 | Hnr protein [impor | 365 | 6 | 3.1 | 402 | 2 | F90035 | histidine-tRNA lig |
| 293 | 6 | 3.1 | 337 | 2 | A36871 | 37K regulator resp | 366 | 6 | 3.1 | 403 | 1 | G70311 | pyruvate dehydrog |
| 294 | 6 | 3.1 | 339 | 2 | B69436 | LSU ribosomal prot | 367 | 6 | 3.1 | 406 | 2 | T24273 | hypothetical prote |
| 295 | 6 | 3.1 | 339 | 2 | UC7712 | transcription coac | 368 | 6 | 3.1 | 407 | 2 | F69865 | conserved hypothet |
| 296 | 6 | 3.1 | 340 | 2 | E69507 | signal recognition | 369 | 6 | 3.1 | 407 | 2 | AB0077 | probable aminotran |
| 297 | 6 | 3.1 | 340 | 2 | T09416 | coil protein P022, | 370 | 6 | 3.1 | 410 | 2 | H72502 | hypothetical prote |
| 298 | 6 | 3.1 | 340 | 2 | T01949 | hypothetical prote | 371 | 6 | 3.1 | 410 | 2 | S29129 | calreticulin precu |
| 299 | 6 | 3.1 | 340 | 2 | AH1103 | arginine kinase ho | 372 | 6 | 3.1 | 411 | 2 | A70509 | hypothetical prote |
| 300 | 6 | 3.1 | 340 | 2 | AH1465 | transcription regu | 373 | 6 | 3.1 | 411 | 2 | A34939 | transforming growt |
| 301 | 6 | 3.1 | 341 | 1 | RPECTT | probable N-acetyl | 374 | 6 | 3.1 | 412 | 2 | T17531 | proline-rich prote |
| 302 | 6 | 3.1 | 341 | 2 | S51285 | transcription regu | 375 | 6 | 3.1 | 412 | 2 | A83604 | probable MFS trans |
| 303 | 6 | 3.1 | 341 | 2 | E91236 | transcription regu | 376 | 6 | 3.1 | 412 | 2 | C69160 | phosphoenolpyruvat |
| 304 | 6 | 3.1 | 341 | 2 | B60083 | dihydroorotase (EC | 377 | 6 | 3.1 | 413 | 2 | F75087 | purine-cytosine pe |
| 305 | 6 | 3.1 | 342 | 2 | S76410 | probable acidic ri | 378 | 6 | 3.1 | 414 | 2 | T22539 | hypothetical prote |
| 306 | 6 | 3.1 | 342 | 2 | G71216 | hypothetical prote | 379 | 6 | 3.1 | 414 | 2 | A39205 | nuclear localizati |
| 307 | 6 | 3.1 | 344 | 2 | T22182 | galactitol-1-phosp | 380 | 6 | 3.1 | 414 | 2 | D87448 | peptidase, M20/M25 |
| 308 | 6 | 3.1 | 346 | 1 | B64976 | galactitol-1-phosp | 381 | 6 | 3.1 | 414 | 2 | A69307 | cell wall-binding |
| 309 | 6 | 3.1 | 346 | 2 | H81915 | probable alcohol d | 382 | 6 | 3.1 | 414 | 2 | C96793 | unknown protein F1 |
| 310 | 6 | 3.1 | 346 | 2 | F90990 | galactitol-1-phosp | 383 | 6 | 3.1 | 415 | 2 | A47033 | chloramphenicol re |
| 311 | 6 | 3.1 | 346 | 2 | H85835 | galactitol-1-phosp | 384 | 6 | 3.1 | 419 | 2 | JQ1201 | CmlA protein - Pse |
| 312 | 6 | 3.1 | 346 | 2 | H72237 | hypothetical prote | 385 | 6 | 3.1 | 419 | 2 | E69888 | DNA primase chain |
| 313 | 6 | 3.1 | 346 | 2 | A83725 | hypothetical prote | 386 | 6 | 3.1 | 420 | 2 | S45630 | multidrug resistant |
| 314 | 6 | 3.1 | 347 | 2 | G83026 | chemotaxis protein | 387 | 6 | 3.1 | 420 | 2 | T45592 | hypothetical prote |
| 315 | 6 | 3.1 | 347 | 2 | T24921 | hypothetical prote | 388 | 6 | 3.1 | 420 | 2 | C84201 | conserved hypothet |
| 316 | 6 | 3.1 | 348 | 1 | H81186 | probable alcohol d | 389 | 6 | 3.1 | 420 | 2 | T41236 | phosphoglycerate k |
| 317 | 6 | 3.1 | 349 | 1 | E64442 | probable arsenical | 390 | 6 | 3.1 | 421 | 2 | A24830 | hypothetical outer |
| 318 | 6 | 3.1 | 349 | 2 | E89795 | conserved hypothet | 391 | 6 | 3.1 | 421 | 2 | D95975 | probable cytosine |
| 319 | 6 | 3.1 | 349 | 2 | JH0235 | hypothetical 39K p | 392 | 6 | 3.1 | 422 | 2 | A71058 | macrolide-efflux p |
| 320 | 6 | 3.1 | 350 | 1 | K1BEPF | thymidine kinase (| 393 | 6 | 3.1 | 422 | 2 | C70046 | |
| 321 | 6 | 3.1 | 352 | 2 | G86660 | adenosine deaminas | 394 | 6 | 3.1 | 422 | 2 | | |

| | | | | | | | | | | | | |
|-----|---|-----|-----|---|--------|---------------------|-----|---|-----|---|--------|---------------------|
| 395 | 6 | 3.1 | 427 | 2 | G59067 | N-ethylammine ch | 468 | 1 | 502 | 1 | S45039 | cytochrome P450 - |
| 396 | 6 | 3.1 | 427 | 2 | A1131 | permeases homolog | 469 | 6 | 502 | 2 | A84582 | hexokinase (ATHXK2 |
| 397 | 6 | 3.1 | 427 | 2 | A11491 | permeases homolog | 470 | 6 | 504 | 2 | S31190 | phase-1 flagellin |
| 398 | 6 | 3.1 | 427 | 2 | S38032 | hypothetical prote | 471 | 6 | 505 | 2 | B64560 | poly E-rich protei |
| 399 | 6 | 3.1 | 428 | 2 | T47400 | hypothetical prote | 472 | 6 | 505 | 2 | S75961 | NADH2 dehydrogenas |
| 400 | 6 | 3.1 | 429 | 1 | S18489 | phosphoribosylamin | 473 | 6 | 507 | 2 | S33192 | phase-1 flagellin |
| 401 | 6 | 3.1 | 429 | 2 | AC0391 | phosphoribosylglyc | 474 | 6 | 507 | 2 | S33185 | phase-1 flagellin |
| 402 | 6 | 3.1 | 430 | 2 | D22402 | UDP-N-acetylmuramo | 475 | 6 | 507 | 2 | T48645 | glycine betaine tr |
| 403 | 6 | 3.1 | 430 | 2 | AD0138 | tolB colicin impor | 476 | 6 | 507 | 2 | AD1336 | glycine betaine tr |
| 404 | 6 | 3.1 | 431 | 2 | G75108 | pyridoxal-phosphat | 477 | 6 | 507 | 2 | G87466 | tryptophan halogen |
| 405 | 6 | 3.1 | 431 | 2 | G75108 | probable aspartoki | 478 | 6 | 508 | 2 | A53465 | phase 1 flagellin |
| 406 | 6 | 3.1 | 431 | 2 | G84276 | hypothetical prote | 479 | 6 | 508 | 2 | E72299 | glutamate synthase |
| 407 | 6 | 3.1 | 431 | 2 | F84375 | N-ethylammine ch | 480 | 6 | 509 | 2 | T06300 | hypothetical prote |
| 408 | 6 | 3.1 | 431 | 2 | UC7730 | 1-aminocyclopropan | 481 | 6 | 509 | 2 | G96552 | unknown protein, 6 |
| 409 | 6 | 3.1 | 433 | 2 | S37790 | probable serine/th | 482 | 6 | 510 | 2 | G76369 | tryptophan halogen |
| 410 | 6 | 3.1 | 435 | 2 | AB2554 | conserved hypothet | 483 | 6 | 511 | 2 | T36306 | hypothetical prote |
| 411 | 6 | 3.1 | 436 | 2 | T30911 | xylanase (EC 3.2.1 | 484 | 6 | 512 | 2 | S75887 | probable anthranil |
| 412 | 6 | 3.1 | 437 | 1 | B69448 | ribulose-bisphosph | 485 | 6 | 513 | 1 | A47436 | 1,25-dihydroxyvita |
| 413 | 6 | 3.1 | 438 | 2 | E87616 | hypothetical prote | 486 | 6 | 513 | 2 | S75997 | asparagine-tRNA li |
| 414 | 6 | 3.1 | 438 | 2 | S64917 | hypothetical prote | 487 | 6 | 513 | 2 | A51154 | sodium/solute symp |
| 415 | 6 | 3.1 | 440 | 2 | IS5442 | peroxisome prolif | 488 | 6 | 519 | 2 | AH0064 | thiamin transport |
| 416 | 6 | 3.1 | 440 | 2 | UC4530 | peroxisome prolif | 489 | 6 | 525 | 2 | G84406 | halolysin [impor |
| 417 | 6 | 3.1 | 440 | 2 | T43198 | nitrilase/Fhlt pro | 490 | 6 | 525 | 2 | B82293 | MvIN protein [VCO68 |
| 418 | 6 | 3.1 | 440 | 2 | B71153 | hypothetical prote | 491 | 6 | 526 | 2 | C84223 | methylmalonyl-CoA |
| 419 | 6 | 3.1 | 441 | 2 | A45360 | steroid hormone re | 492 | 6 | 526 | 2 | A75581 | flavin monochrome o |
| 420 | 6 | 3.1 | 443 | 2 | T14916 | mitosis-specific c | 493 | 6 | 528 | 2 | T34417 | delayed rectifier |
| 421 | 6 | 3.1 | 444 | 2 | B83249 | conserved hypothet | 494 | 6 | 529 | 1 | VGNZSP | cell fusion glycop |
| 422 | 6 | 3.1 | 445 | 2 | A48947 | glutamate-ammonia | 495 | 6 | 530 | 2 | T42234 | cof head-related |
| 423 | 6 | 3.1 | 445 | 2 | JQ0422 | beta-tubulin 1 - a | 496 | 6 | 531 | 2 | T16263 | hypothetical prote |
| 424 | 6 | 3.1 | 445 | 2 | H88244 | protein T01B7.5 (i | 497 | 6 | 531 | 2 | B70400 | phage related prot |
| 425 | 6 | 3.1 | 446 | 2 | T03021 | mitosis-specific c | 498 | 6 | 531 | 2 | F84398 | phosphate ABC tran |
| 426 | 6 | 3.1 | 447 | 2 | T02547 | hypothetical prote | 499 | 6 | 534 | 2 | S61185 | hypothetical prote |
| 427 | 6 | 3.1 | 447 | 2 | T36597 | hypothetical prote | 500 | 6 | 535 | 2 | F81094 | pyruvate dehydroge |
| 428 | 6 | 3.1 | 448 | 2 | F84241 | hypothetical prote | 501 | 6 | 535 | 2 | B82358 | alkaline serine pr |
| 429 | 6 | 3.1 | 449 | 2 | T36042 | probable plasmid r | 502 | 6 | 535 | 2 | F81847 | dihydrolipoamide S |
| 430 | 6 | 3.1 | 452 | 2 | T05699 | hypothetical prote | 503 | 6 | 536 | 1 | C64728 | probable membrane |
| 431 | 6 | 3.1 | 452 | 2 | D86759 | hypothetical prote | 504 | 6 | 536 | 2 | G85488 | probable transport |
| 432 | 6 | 3.1 | 453 | 2 | A97431 | alpha-glucosidase-b | 505 | 6 | 536 | 2 | G90637 | probable transport |
| 433 | 6 | 3.1 | 453 | 2 | AB2649 | hypothetical prote | 506 | 6 | 536 | 2 | AH0515 | probable ABC trans |
| 434 | 6 | 3.1 | 454 | 2 | T02593 | hypothetical prote | 507 | 6 | 542 | 2 | T06728 | pectate lyase (EC |
| 435 | 6 | 3.1 | 455 | 2 | G75473 | probable carotenol | 508 | 6 | 546 | 2 | S67292 | probable membrane |
| 436 | 6 | 3.1 | 458 | 2 | H82504 | conserved hypothet | 509 | 6 | 552 | 2 | S46809 | hypothetical prote |
| 437 | 6 | 3.1 | 459 | 2 | C81195 | spermidine/putresc | 510 | 6 | 552 | 2 | E72283 | alpha-galactosidas |
| 438 | 6 | 3.1 | 460 | 2 | A39338 | phosphotransferase | 511 | 6 | 555 | 2 | C72512 | probable thermosom |
| 439 | 6 | 3.1 | 460 | 2 | G90890 | hypothetical prote | 512 | 6 | 556 | 2 | A6024 | neurofilament-l su |
| 440 | 6 | 3.1 | 460 | 2 | B85727 | hypothetical prote | 513 | 6 | 559 | 2 | AG2471 | two-component sens |
| 441 | 6 | 3.1 | 460 | 2 | E64902 | hypothetical prote | 514 | 6 | 560 | 1 | F69059 | arginine-tRNA liga |
| 442 | 6 | 3.1 | 461 | 2 | G59093 | hypothetical prote | 515 | 6 | 560 | 2 | T52438 | PRM1 homolog [impo |
| 443 | 6 | 3.1 | 461 | 2 | A60746 | chromogranin A pre | 516 | 6 | 562 | 2 | S78099 | furostanol glycosi |
| 444 | 6 | 3.1 | 462 | 1 | T26195 | hypothetical prote | 517 | 6 | 562 | 2 | E64412 | hypothetical prote |
| 445 | 6 | 3.1 | 467 | 2 | A60746 | hypothetical prote | 518 | 6 | 562 | 2 | S75308 | DNA ligase (EC 6.5 |
| 446 | 6 | 3.1 | 469 | 2 | T02325 | probable selenium- | 519 | 6 | 565 | 2 | T47775 | methyl-accepting c |
| 447 | 6 | 3.1 | 470 | 2 | A49499 | metalloelastase HM | 520 | 6 | 569 | 2 | F70332 | proline-tRNA synth |
| 448 | 6 | 3.1 | 470 | 2 | T52440 | PRM1 homolog [impo | 521 | 6 | 570 | 2 | S07330 | serine/threonine p |
| 449 | 6 | 3.1 | 470 | 2 | AB2266 | ammonium transport | 522 | 6 | 570 | 2 | S42866 | proline-tRNA ligas |
| 450 | 6 | 3.1 | 471 | 2 | AB2266 | trigger factor [im | 523 | 6 | 572 | 2 | B84958 | NADH2 dehydrogenas |
| 451 | 6 | 3.1 | 471 | 2 | D83388 | probable MFS trans | 524 | 6 | 574 | 2 | S58992 | hypothetical prote |
| 452 | 6 | 3.1 | 471 | 2 | S05392 | hypothetical prote | 525 | 6 | 575 | 2 | T34280 | hypothetical prote |
| 453 | 6 | 3.1 | 476 | 2 | AF0765 | undecaprenyl-phosp | 526 | 6 | 577 | 2 | T22460 | cell division cycl |
| 454 | 6 | 3.1 | 482 | 1 | ZPBX | mitochondrial proc | 527 | 6 | 579 | 2 | T13004 | Rubisco subunit bi |
| 455 | 6 | 3.1 | 482 | 1 | AB2515 | hypothetical prote | 528 | 6 | 580 | 2 | C96597 | fibulin-1D precurs |
| 456 | 6 | 3.1 | 483 | 2 | T20895 | hypothetical prote | 529 | 6 | 580 | 2 | T43210 | fibulin-1D precurs |
| 457 | 6 | 3.1 | 483 | 2 | S43737 | protein kinase SLR | 530 | 6 | 589 | 2 | A29904 | serine proteinase, |
| 458 | 6 | 3.1 | 484 | 2 | G81363 | probable amino-aci | 531 | 6 | 590 | 2 | A75474 | probable thiol-dis |
| 459 | 6 | 3.1 | 488 | 2 | G95105 | lysine decarboxyla | 532 | 6 | 591 | 2 | E83039 | calnexin - human |
| 460 | 6 | 3.1 | 491 | 2 | H97973 | lysine decarboxyla | 533 | 6 | 591 | 2 | E83039 | calnexin precursor |
| 461 | 6 | 3.1 | 491 | 2 | C96585 | hypothetical prote | 534 | 6 | 592 | 2 | A6673 | calnexin precursor |
| 462 | 6 | 3.1 | 492 | 1 | S68968 | trypanothione-disu | 535 | 6 | 592 | 2 | A37273 | arginyl-tRNA synth |
| 463 | 6 | 3.1 | 492 | 1 | S28003 | trypanothione-disu | 536 | 6 | 593 | 1 | E87665 | pyruvate, phosphat |
| 464 | 6 | 3.1 | 492 | 2 | T06875 | preproteins translo | 537 | 6 | 600 | 2 | E87028 | transport protein |
| 465 | 6 | 3.1 | 494 | 1 | WJFEBC | homeotic protein b | 538 | 6 | 601 | 2 | E87028 | transport protein |
| 466 | 6 | 3.1 | 494 | 2 | E83254 | glutamyl-tRNA synt | 539 | 6 | 603 | 2 | B83022 | probable transcarb |
| 467 | 6 | 3.1 | 498 | 2 | PC6300 | synaptotagmin X - | 540 | 6 | 607 | 2 | F82966 | |
| | | | | | | xylan 1,4-beta-xy | | | | | | |

| | | | | | | | | | | | | | |
|-----|---|-----|-----|---|--------|--------------------|-----|---|-----|------|---|--------|----------------------|
| 541 | 6 | 3.1 | 608 | 2 | T19437 | hypothetical prote | 614 | 6 | 3.1 | 755 | 2 | T47806 | hypothetical prote |
| 542 | 6 | 3.1 | 611 | 2 | D81347 | arginine decarboxy | 615 | 6 | 3.1 | 758 | 2 | T02925 | protoporphyrin IX |
| 543 | 6 | 3.1 | 611 | 2 | T20501 | hypothetical prote | 616 | 6 | 3.1 | 758 | 2 | A98290 | expolysaccharide |
| 544 | 6 | 3.1 | 611 | 2 | F70325 | conserved hypotet | 617 | 6 | 3.1 | 758 | 2 | AB2994 | hypothetical prote |
| 545 | 6 | 3.1 | 612 | 2 | T11628 | MVP1 protein - fls | 618 | 6 | 3.1 | 760 | 2 | T24521 | hypothetical prote |
| 546 | 6 | 3.1 | 613 | 2 | S57687 | probable membrane | 619 | 6 | 3.1 | 763 | 2 | T08929 | hypothetical prote |
| 547 | 6 | 3.1 | 614 | 1 | QRECBT | vitamin B12 recept | 620 | 6 | 3.1 | 768 | 2 | G82506 | GTP pyrophosphokin |
| 548 | 6 | 3.1 | 614 | 2 | A98241 | hypothetical prote | 621 | 6 | 3.1 | 769 | 2 | D81828 | structural polypro |
| 549 | 6 | 3.1 | 614 | 2 | AB8088 | hypothetical prote | 622 | 6 | 3.1 | 773 | 2 | A47666 | xylosidase - Therm |
| 550 | 6 | 3.1 | 614 | 2 | AB0935 | vitamin B12 recept | 623 | 6 | 3.1 | 778 | 2 | D72421 | sporulation protei |
| 551 | 6 | 3.1 | 614 | 2 | S27962 | modulator recognit | 624 | 6 | 3.1 | 778 | 2 | S43132 | probable polyprote |
| 552 | 6 | 3.1 | 618 | 1 | S38004 | probable transp | 625 | 6 | 3.1 | 778 | 2 | D85055 | formate dehydrogen |
| 553 | 6 | 3.1 | 618 | 2 | A83074 | hypothetical prote | 626 | 6 | 3.1 | 782 | 2 | B83966 | hypothetical prote |
| 554 | 6 | 3.1 | 619 | 2 | T34451 | hypothetical prote | 627 | 6 | 3.1 | 786 | 2 | T26811 | hypothetical prote |
| 555 | 6 | 3.1 | 621 | 2 | S73155 | hypothetical prote | 628 | 6 | 3.1 | 786 | 2 | F70735 | hypothetical prote |
| 556 | 6 | 3.1 | 622 | 2 | T37204 | hypothetical prote | 629 | 6 | 3.1 | 792 | 2 | S72831 | cadherin 12 - huma |
| 557 | 6 | 3.1 | 622 | 2 | C84506 | probable Achila re | 630 | 6 | 3.1 | 794 | 2 | I59372 | hypothetical prote |
| 558 | 6 | 3.1 | 622 | 2 | AC1236 | acyltransferase (c | 631 | 6 | 3.1 | 802 | 2 | T05596 | probable potassium |
| 559 | 6 | 3.1 | 627 | 2 | B44409 | gamma-aminobutyric | 632 | 6 | 3.1 | 805 | 2 | E70474 | translation initia |
| 560 | 6 | 3.1 | 627 | 2 | JH0695 | probable biotin-pr | 633 | 6 | 3.1 | 805 | 2 | A10176 | probable oxidoredu |
| 561 | 6 | 3.1 | 631 | 2 | T40189 | hypothetical prote | 634 | 6 | 3.1 | 805 | 2 | T40275 | probable glutaminy |
| 562 | 6 | 3.1 | 633 | 2 | T52506 | hypothetical prote | 635 | 6 | 3.1 | 811 | 2 | F71880 | unknown protein [i |
| 563 | 6 | 3.1 | 633 | 2 | G96503 | protein F9C16.15 [| 636 | 6 | 3.1 | 815 | 2 | F71880 | probable ATP-depen |
| 564 | 6 | 3.1 | 633 | 2 | AH1598 | acyltransferase (c | 637 | 6 | 3.1 | 816 | 2 | D96544 | probable ATP-depen |
| 565 | 6 | 3.1 | 634 | 2 | C69975 | acyltransferase ho | 638 | 6 | 3.1 | 817 | 2 | F83073 | heat shock protein |
| 566 | 6 | 3.1 | 638 | 2 | S51266 | trsg protein - Yer | 639 | 6 | 3.1 | 823 | 2 | T09882 | adipocyte transcri |
| 567 | 6 | 3.1 | 638 | 2 | T73709 | flr-1 protein - Ca | 640 | 6 | 3.1 | 845 | 2 | JC5256 | probable transcrip |
| 568 | 6 | 3.1 | 638 | 2 | T44763 | conserved hypotet | 641 | 6 | 3.1 | 857 | 2 | T40824 | neurofilament trip |
| 569 | 6 | 3.1 | 639 | 2 | D70720 | hypothetical prote | 642 | 6 | 3.1 | 858 | 2 | S15762 | chitinase (EC 3.2. |
| 570 | 6 | 3.1 | 641 | 2 | PH1919 | FL-160-4 protein - | 643 | 6 | 3.1 | 860 | 2 | JC4566 | lipoxxygenase (EC 1 |
| 571 | 6 | 3.1 | 644 | 2 | S55395 | neurofilament prot | 644 | 6 | 3.1 | 864 | 1 | S07075 | hypothetical prote |
| 572 | 6 | 3.1 | 646 | 2 | T11599 | hypothetical prote | 645 | 6 | 3.1 | 868 | 2 | G71691 | ATP-dependent RNA |
| 573 | 6 | 3.1 | 646 | 2 | UC5583 | 85K SH3 domain-con | 646 | 6 | 3.1 | 873 | 2 | F71092 | ubiquitin-specific |
| 574 | 6 | 3.1 | 652 | 2 | I48083 | amphotropic murine | 647 | 6 | 3.1 | 875 | 2 | T50182 | allanyl-tRNA synth |
| 575 | 6 | 3.1 | 657 | 2 | C89815 | methionyl-tRNA syn | 648 | 6 | 3.1 | 881 | 2 | A97107 | spindle pole body- |
| 576 | 6 | 3.1 | 659 | 1 | B44212 | structural protein | 649 | 6 | 3.1 | 882 | 2 | T43250 | DNA-directed RNA p |
| 577 | 6 | 3.1 | 659 | 2 | T33557 | hypothetical prote | 650 | 6 | 3.1 | 885 | 1 | S26723 | probable adenylate |
| 578 | 6 | 3.1 | 660 | 1 | VHWH2 | structural protein | 651 | 6 | 3.1 | 886 | 2 | T40734 | hypothetical prote |
| 579 | 6 | 3.1 | 660 | 2 | T45569 | receptor protein k | 652 | 6 | 3.1 | 891 | 2 | B97759 | cell wall-associated |
| 580 | 6 | 3.1 | 664 | 2 | D96633 | hypothetical prote | 653 | 6 | 3.1 | 894 | 2 | F69730 | hypothetical prote |
| 581 | 6 | 3.1 | 670 | 1 | H70421 | hypothetical prote | 654 | 6 | 3.1 | 897 | 2 | S50550 | aconitate hydratase |
| 582 | 6 | 3.1 | 670 | 2 | G72742 | hypothetical prote | 655 | 6 | 3.1 | 901 | 2 | F89910 | DNA polymerase I (|
| 583 | 6 | 3.1 | 674 | 2 | T06720 | hypothetical prote | 656 | 6 | 3.1 | 908 | 2 | C70168 | hypothetical prote |
| 584 | 6 | 3.1 | 676 | 1 | S69783 | outer membrane pro | 657 | 6 | 3.1 | 909 | 2 | G69599 | aconitate hydratase |
| 585 | 6 | 3.1 | 680 | 2 | T19939 | hypothetical prote | 658 | 6 | 3.1 | 911 | 2 | T18451 | hypothetical prote |
| 586 | 6 | 3.1 | 683 | 2 | D90327 | n-methylhydantoina | 659 | 6 | 3.1 | 912 | 2 | A54423 | brevican precursor |
| 587 | 6 | 3.1 | 689 | 2 | T42760 | fibulin, splice fo | 660 | 6 | 3.1 | 913 | 2 | T52485 | neurofilament prot |
| 588 | 6 | 3.1 | 690 | 2 | A83441 | potassium-transpor | 661 | 6 | 3.1 | 914 | 2 | T17233 | serine/threonine p |
| 589 | 6 | 3.1 | 693 | 2 | T13175 | NADH2 dehydrogenas | 662 | 6 | 3.1 | 915 | 2 | T51600 | hypothetical prote |
| 590 | 6 | 3.1 | 699 | 2 | S67773 | hypothetical prote | 663 | 6 | 3.1 | 942 | 2 | C96574 | pyruvate, phosphat |
| 591 | 6 | 3.1 | 708 | 2 | S70834 | transcription init | 664 | 6 | 3.1 | 946 | 2 | A96748 | metal-transporting |
| 592 | 6 | 3.1 | 709 | 2 | D92825 | conserved hypotet | 665 | 6 | 3.1 | 949 | 2 | T06003 | MitC1 protein - yea |
| 593 | 6 | 3.1 | 711 | 2 | T27358 | hypothetical prote | 666 | 6 | 3.1 | 950 | 2 | S64405 | hypothetical prote |
| 594 | 6 | 3.1 | 712 | 2 | T42990 | fibulin 1, splice | 667 | 6 | 3.1 | 971 | 2 | T24866 | hypothetical prote |
| 595 | 6 | 3.1 | 714 | 2 | A83314 | probable chemotaxi | 668 | 6 | 3.1 | 974 | 2 | T14076 | probable villin li |
| 596 | 6 | 3.1 | 715 | 2 | D85087 | hypothetical prote | 669 | 6 | 3.1 | 996 | 2 | T47518 | serine/threonine p |
| 597 | 6 | 3.1 | 723 | 2 | T47613 | ABC transporter-li | 670 | 6 | 3.1 | 1003 | 2 | F81731 | glycyl-tRNA synthe |
| 598 | 6 | 3.1 | 724 | 2 | S42868 | serine/threonine p | 671 | 6 | 3.1 | 1003 | 2 | B71469 | glycine-tRNA ligase |
| 599 | 6 | 3.1 | 726 | 2 | B86202 | hypothetical prote | 672 | 6 | 3.1 | 1004 | 2 | A55142 | myosin-light-chain |
| 600 | 6 | 3.1 | 728 | 1 | HHCH90 | heat shock protein | 673 | 6 | 3.1 | 1017 | 2 | T37201 | hypothetical prote |
| 601 | 6 | 3.1 | 731 | 2 | T08855 | nephrocystin - hum | 674 | 6 | 3.1 | 1021 | 2 | B85023 | probable membrane |
| 602 | 6 | 3.1 | 733 | 2 | S31288 | hypothetical prote | 675 | 6 | 3.1 | 1025 | 2 | S54044 | probable GTPase ac |
| 603 | 6 | 3.1 | 735 | 2 | G02937 | fertilin beta - cr | 676 | 6 | 3.1 | 1031 | 2 | T38411 | hypothetical prote |
| 604 | 6 | 3.1 | 735 | 2 | T49622 | hypothetical prote | 677 | 6 | 3.1 | 1033 | 2 | T42701 | hypothetical prote |
| 605 | 6 | 3.1 | 735 | 2 | S74209 | multifunctional be | 678 | 6 | 3.1 | 1036 | 2 | A57386 | large structural p |
| 606 | 6 | 3.1 | 736 | 2 | G01522 | acidic 82 kDa prot | 679 | 6 | 3.1 | 1038 | 2 | S25222 | serine/threonine-s |
| 607 | 6 | 3.1 | 736 | 2 | S59136 | estradiol 17beta-d | 680 | 6 | 3.1 | 1048 | 1 | XP2EA9 | retrovirus-related |
| 608 | 6 | 3.1 | 737 | 2 | F81049 | GTP pyrophosphokin | 681 | 6 | 3.1 | 1051 | 1 | JW0051 | arachidonate 8-lip |
| 609 | 6 | 3.1 | 740 | 2 | T09480 | hypothetical prote | 682 | 6 | 3.1 | 1059 | 2 | B24872 | SKI2 protein homol |
| 610 | 6 | 3.1 | 740 | 2 | T26140 | hypothetical prote | 683 | 6 | 3.1 | 1066 | 2 | T30903 | cobN protein homol |
| 611 | 6 | 3.1 | 748 | 2 | A64319 | carbon-monoxide de | 684 | 6 | 3.1 | 1073 | 1 | S56822 | |
| 612 | 6 | 3.1 | 752 | 2 | S64750 | probable ATP-depen | 685 | 6 | 3.1 | 1085 | 2 | T03531 | |
| 613 | 6 | 3.1 | 754 | 2 | A84473 | probable serine pr | 686 | 6 | 3.1 | | | | |

| | | | | | | | | | | | | |
|-----|-----|------|---|--------|--------------------|-----|---|-----|----|---|--------|---------------------|
| 687 | 3.1 | 1087 | 2 | T30330 | gelsolin-related p | 760 | 5 | 2.6 | 24 | 2 | S02073 | photosystem II 10K |
| 688 | 3.1 | 1087 | 2 | T31100 | probable potassium | 761 | 5 | 2.6 | 27 | 4 | JE0015 | probable 2.8K prot |
| 689 | 3.1 | 1110 | 2 | I51116 | NF-180 - sea lamp | 762 | 5 | 2.6 | 33 | 2 | T06843 | probable plastocqui |
| 690 | 3.1 | 1112 | 2 | T40382 | dna repair protein | 763 | 5 | 2.6 | 36 | 2 | S38517 | mablin II chain |
| 691 | 3.1 | 1113 | 2 | T00736 | hypothetical prote | 764 | 5 | 2.6 | 36 | 2 | A60343 | transferrin prote |
| 692 | 3.1 | 1113 | 2 | S30301 | excision repair pr | 765 | 5 | 2.6 | 43 | 1 | I39482 | MSL leader peptide |
| 693 | 3.1 | 1113 | 2 | T49517 | p63 related protei | 766 | 5 | 2.6 | 43 | 1 | C25028 | hypothetical eryth |
| 694 | 3.1 | 1132 | 2 | T03844 | telomerase catalyt | 767 | 5 | 2.6 | 43 | 1 | S49317 | MSL leader peptide |
| 695 | 3.1 | 1148 | 2 | S51855 | probable catalyt | 768 | 5 | 2.6 | 43 | 1 | I40879 | hypothetical prote |
| 696 | 3.1 | 1163 | 2 | F84669 | probable chromosom | 769 | 5 | 2.6 | 45 | 2 | T52276 | R2R3-MVB transcrip |
| 697 | 3.1 | 1186 | 2 | DNBBEG | DNA-binding protei | 770 | 5 | 2.6 | 45 | 2 | S28838 | RNA-binding protei |
| 698 | 3.1 | 1192 | 2 | T13424 | hypothetical prote | 771 | 5 | 2.6 | 46 | 2 | AF1063 | hypothetical prote |
| 699 | 3.1 | 1197 | 2 | A48350 | DNA-binding protei | 772 | 5 | 2.6 | 47 | 2 | A37174 | dihydrofolate redu |
| 700 | 3.1 | 1201 | 2 | H69898 | hypothetical prote | 773 | 5 | 2.6 | 50 | 2 | T20498 | hypothetical prote |
| 701 | 3.1 | 1209 | 2 | AH2052 | hypothetical prote | 774 | 5 | 2.6 | 51 | 2 | T30904 | streptococci A-Fr |
| 702 | 3.1 | 1246 | 2 | JQ0406 | hypothetical prote | 775 | 5 | 2.6 | 51 | 2 | T35701 | hypothetical prote |
| 703 | 3.1 | 1257 | 2 | I58383 | retinoblastoma bin | 776 | 5 | 2.6 | 54 | 2 | C71570 | probable serine pr |
| 704 | 3.1 | 1257 | 2 | T09493 | period protein hom | 777 | 5 | 2.6 | 54 | 2 | T36552 | hypothetical prote |
| 705 | 3.1 | 1264 | 2 | H96498 | hypothetical prote | 778 | 5 | 2.6 | 55 | 2 | D32052 | hypothetical prote |
| 706 | 3.1 | 1270 | 2 | T22615 | hypothetical prote | 779 | 5 | 2.6 | 55 | 2 | A82912 | fixs protein - Rhi |
| 707 | 3.1 | 1271 | 2 | T08607 | hypothetical prote | 780 | 5 | 2.6 | 55 | 2 | B95344 | ribosomal protein |
| 708 | 3.1 | 1282 | 2 | JE0120 | glycoprotein A - m | 781 | 5 | 2.6 | 55 | 2 | E81417 | fixs1 nitrogen fix |
| 709 | 3.1 | 1290 | 2 | S73653 | DNA-directed RNA p | 782 | 5 | 2.6 | 55 | 2 | B97548 | small hydrophobic |
| 710 | 3.1 | 1298 | 2 | I54367 | X-linked nuclear p | 783 | 5 | 2.6 | 55 | 2 | I53423 | MHC class II DOB2 |
| 711 | 3.1 | 1333 | 2 | B84601 | probable retroelem | 784 | 5 | 2.6 | 56 | 2 | S74259 | tropomyosin 3, fast |
| 712 | 3.1 | 1337 | 2 | T13948 | atypical protein k | 785 | 5 | 2.6 | 56 | 2 | T34739 | hydrophobic protei |
| 713 | 3.1 | 1351 | 2 | C71607 | hypothetical prote | 786 | 5 | 2.6 | 56 | 2 | JW0095 | P5 protein - human |
| 714 | 3.1 | 1353 | 2 | T00347 | hypothetical prote | 787 | 5 | 2.6 | 56 | 2 | AD2498 | hypothetical prote |
| 715 | 3.1 | 1357 | 2 | T29465 | hypothetical prote | 788 | 5 | 2.6 | 58 | 2 | T43241 | probable ribosomal |
| 716 | 3.1 | 1367 | 2 | T38820 | probable calcium-c | 789 | 5 | 2.6 | 58 | 2 | E36595 | unknown protein, 2 |
| 717 | 3.1 | 1386 | 2 | T00257 | hypothetical prote | 790 | 5 | 2.6 | 58 | 2 | S58143 | gene 14 protein - |
| 718 | 3.1 | 1388 | 2 | A57655 | tim (timeless) pro | 791 | 5 | 2.6 | 58 | 2 | A45824 | ribosomal protein |
| 719 | 3.1 | 1426 | 2 | A99580 | hypothetical prote | 792 | 5 | 2.6 | 59 | 2 | AE1777 | ribosomal protein |
| 720 | 3.1 | 1436 | 2 | JC5290 | protein-tyrosine-p | 793 | 5 | 2.6 | 59 | 2 | AF1401 | hypothetical prote |
| 721 | 3.1 | 1442 | 2 | S72441 | protein-tyrosine-p | 794 | 5 | 2.6 | 59 | 2 | D82505 | hypothetical prote |
| 722 | 3.1 | 1458 | 2 | T51995 | hypothetical prote | 795 | 5 | 2.6 | 60 | 2 | B82207 | hypothetical prote |
| 723 | 3.1 | 1458 | 2 | T39266 | probable cell cycl | 796 | 5 | 2.6 | 60 | 2 | G97044 | 60S ribosomal prot |
| 724 | 3.1 | 1553 | 2 | T03301 | rab3 effector cycl | 797 | 5 | 2.6 | 61 | 2 | T40671 | YlcE protein - Esc |
| 725 | 3.1 | 1558 | 2 | B71603 | RESA-H3 antigen PF | 798 | 5 | 2.6 | 62 | 2 | A64789 | aquaporin - common |
| 726 | 3.1 | 1583 | 2 | S59644 | sister chromatid c | 799 | 5 | 2.6 | 62 | 2 | T13997 | hypothetical prote |
| 727 | 3.1 | 1584 | 2 | T00026 | brain-specific ang | 800 | 5 | 2.6 | 62 | 2 | H64443 | hypothetical prote |
| 728 | 3.1 | 1641 | 2 | T38614 | helicase II - huma | 801 | 5 | 2.6 | 62 | 2 | S40758 | neurotoxin X - sco |
| 729 | 3.1 | 1743 | 2 | T26859 | complement C4A pre | 802 | 5 | 2.6 | 65 | 2 | A59222 | hypothetical prote |
| 730 | 3.1 | 1744 | 2 | C4HU | hypothetical prote | 803 | 5 | 2.6 | 66 | 2 | T35138 | hypothetical prote |
| 731 | 3.1 | 2076 | 2 | T28915 | hypothetical prote | 804 | 5 | 2.6 | 66 | 2 | S48660 | M-like protein enn |
| 732 | 3.1 | 2172 | 2 | T20145 | hypothetical prote | 805 | 5 | 2.6 | 67 | 2 | S61817 | tropomyosin 1, fast |
| 733 | 3.1 | 2210 | 2 | RRXPV | genome polyprotein | 806 | 5 | 2.6 | 67 | 2 | G84255 | hypothetical prote |
| 734 | 3.1 | 2254 | 2 | D86215 | protein T6D22.14 (| 807 | 5 | 2.6 | 67 | 2 | I69230 | GPI-anchored epidi |
| 735 | 3.1 | 2257 | 2 | A57710 | acetyl-CoA carboxy | 808 | 5 | 2.6 | 67 | 2 | AB0448 | probable membrane |
| 736 | 3.1 | 2493 | 2 | S26372 | nonstructural poly | 809 | 5 | 2.6 | 67 | 2 | B81328 | hypothetical prote |
| 737 | 3.1 | 2493 | 2 | S72349 | nonstructural poly | 810 | 5 | 2.6 | 67 | 2 | AH1921 | hypothetical prote |
| 738 | 3.1 | 2499 | 2 | A30788 | mannose 6-phosphat | 811 | 5 | 2.6 | 67 | 2 | JC6521 | metallothionein II |
| 739 | 3.1 | 2649 | 2 | A40937 | bullous pemphigoid | 812 | 5 | 2.6 | 68 | 2 | E86945 | hypothetical prote |
| 740 | 3.1 | 2722 | 2 | T20532 | hypothetical prote | 813 | 5 | 2.6 | 69 | 2 | B97230 | hypothetical prote |
| 741 | 3.1 | 2738 | 2 | B88320 | protein F07A11.6 (| 814 | 5 | 2.6 | 69 | 2 | B64497 | hypothetical prote |
| 742 | 3.1 | 3282 | 2 | B82750 | hemagglutinin-like | 815 | 5 | 2.6 | 70 | 2 | G82833 | hypothetical prote |
| 743 | 3.1 | 3286 | 2 | GNWVDF | genome polyprotein | 816 | 5 | 2.6 | 70 | 2 | A59346 | seed storage prote |
| 744 | 3.1 | 3442 | 2 | B82589 | hemagglutinin-like | 817 | 5 | 2.6 | 70 | 2 | S15069 | ribosomal protein |
| 745 | 3.1 | 3455 | 2 | B82519 | hemagglutinin-like | 818 | 5 | 2.6 | 71 | 1 | S15069 | hypothetical prote |
| 746 | 3.1 | 3498 | 2 | T23330 | hypothetical prote | 819 | 5 | 2.6 | 71 | 2 | G84978 | hypothetical prote |
| 747 | 3.1 | 4967 | 2 | S72269 | ryanodine receptor | 820 | 5 | 2.6 | 71 | 2 | G72226 | hypothetical prote |
| 748 | 3.1 | 4969 | 2 | A37113 | ryanodine receptor | 821 | 5 | 2.6 | 71 | 2 | D82541 | hypothetical prote |
| 749 | 3.1 | 5032 | 2 | A35041 | ryanodine receptor | 822 | 5 | 2.6 | 71 | 2 | S78193 | ribosomal protein |
| 750 | 3.1 | 5035 | 2 | I46646 | ryanodine receptor | 823 | 5 | 2.6 | 72 | 2 | S28843 | mablin II chain |
| 751 | 3.1 | 5037 | 2 | B35041 | ryanodine receptor | 824 | 5 | 2.6 | 72 | 2 | S05485 | hypothetical prote |
| 752 | 3.1 | 7829 | 2 | T15789 | hypothetical prote | 825 | 5 | 2.6 | 72 | 2 | B43259 | hypothetical prote |
| 753 | 3.1 | 9376 | 2 | T14593 | syringomycin synth | 826 | 5 | 2.6 | 73 | 2 | H71149 | hypothetical prote |
| 754 | 2.6 | 10 | 2 | E60527 | perm-activating p | 827 | 5 | 2.6 | 73 | 2 | T31216 | hypothetical prote |
| 755 | 2.6 | 10 | 2 | C60588 | sperm-activating p | 828 | 5 | 2.6 | 73 | 2 | F85554 | hypothetical prote |
| 756 | 2.6 | 19 | 2 | JP0057 | ribosomal protein | 829 | 5 | 2.6 | 74 | 2 | C23734 | insulin-like growt |
| 757 | 2.6 | 20 | 2 | S71593 | serine proteinase | 830 | 5 | 2.6 | 74 | 2 | S10868 | hypothetical prote |
| 758 | 2.6 | 20 | 2 | A54077 | cytochrome b558 - | 831 | 5 | 2.6 | 74 | 2 | A43921 | dihydropyridine re |
| 759 | 2.6 | 20 | 2 | JP0056 | ribosomal protein | 832 | 5 | 2.6 | 75 | 2 | S62073 | M-like protein pre |

| | | | | | | | | | | | | |
|-----|-----|----|---|--------|---------------------|-----|---|-----|----|---|--------|--------------------|
| 833 | 2.6 | 75 | 2 | E69508 | conserved hypothet | 906 | 5 | 2.6 | 88 | 2 | A84166 | hypothetical prote |
| 834 | 2.6 | 75 | 2 | C95197 | hypothetical prote | 907 | 5 | 2.6 | 88 | 2 | A83241 | hypothetical prote |
| 835 | 2.6 | 75 | 2 | A86883 | hypothetical prote | 908 | 5 | 2.6 | 88 | 2 | T30626 | hypothetical prote |
| 836 | 2.6 | 75 | 2 | T30286 | hypothetical prote | 909 | 5 | 2.6 | 88 | 2 | D86013 | hypothetical prote |
| 837 | 2.6 | 75 | 2 | H70966 | hypothetical prote | 910 | 5 | 2.6 | 89 | 2 | S38701 | MHC class II histo |
| 838 | 2.6 | 75 | 2 | H98063 | hypothetical prote | 911 | 5 | 2.6 | 89 | 2 | S38702 | MHC class II histo |
| 839 | 2.6 | 75 | 2 | AG2371 | hypothetical prote | 912 | 5 | 2.6 | 89 | 2 | S38704 | MHC class II histo |
| 840 | 2.6 | 76 | 1 | W7LBA4 | E7 protein - bovin | 913 | 5 | 2.6 | 89 | 2 | PL0129 | class II histocomp |
| 841 | 2.6 | 76 | 2 | I68907 | MHC protein - cott | 914 | 5 | 2.6 | 89 | 2 | G53226 | retrovirus-related |
| 842 | 2.6 | 76 | 2 | I68920 | MHC protein - cott | 915 | 5 | 2.6 | 89 | 2 | A90820 | hypothetical prote |
| 843 | 2.6 | 76 | 2 | I68915 | M protein - curt | 916 | 5 | 2.6 | 89 | 2 | T14959 | hypothetical prote |
| 844 | 2.6 | 76 | 2 | S60789 | M protein - curt | 917 | 5 | 2.6 | 90 | 1 | R3RZ15 | ribosomal protein |
| 845 | 2.6 | 76 | 2 | H81214 | hypothetical prote | 918 | 5 | 2.6 | 90 | 1 | R3ZM15 | ribosomal protein |
| 846 | 2.6 | 77 | 2 | E82407 | hypothetical prote | 919 | 5 | 2.6 | 90 | 1 | A34435 | ribosomal protein |
| 847 | 2.6 | 77 | 2 | T35645 | hypothetical prote | 920 | 5 | 2.6 | 90 | 2 | S68801 | acetylcholinestera |
| 848 | 2.6 | 78 | 2 | S72519 | GTP-binding protei | 921 | 5 | 2.6 | 90 | 2 | A24629 | Ig gamma-3 chain C |
| 849 | 2.6 | 78 | 2 | S78474 | GTP-binding protei | 922 | 5 | 2.6 | 90 | 2 | S62081 | M-like protein pre |
| 850 | 2.6 | 78 | 2 | S72518 | GTP-binding protei | 923 | 5 | 2.6 | 90 | 2 | S62081 | hypothetical prote |
| 851 | 2.6 | 78 | 2 | D64590 | hypothetical prote | 924 | 5 | 2.6 | 90 | 2 | B75304 | Ig kappa chain V r |
| 852 | 2.6 | 78 | 2 | B97027 | hypothetical prote | 925 | 5 | 2.6 | 91 | 2 | S17627 | Ig kappa chain V r |
| 853 | 2.6 | 79 | 2 | T07352 | feolA-like protein, | 926 | 5 | 2.6 | 91 | 2 | S17628 | Ig kappa chain V r |
| 854 | 2.6 | 79 | 2 | A90171 | translation initia | 927 | 5 | 2.6 | 91 | 2 | S17629 | Ig kappa chain V r |
| 855 | 2.6 | 79 | 2 | TL7523 | SSU ribosomal prot | 928 | 5 | 2.6 | 91 | 2 | S17637 | Ig kappa chain V r |
| 856 | 2.6 | 79 | 2 | B64614 | hypothetical prote | 929 | 5 | 2.6 | 91 | 2 | S17638 | Ig kappa chain V r |
| 857 | 2.6 | 79 | 2 | C71901 | hypothetical prote | 930 | 5 | 2.6 | 92 | 2 | AB2021 | hypothetical prote |
| 858 | 2.6 | 79 | 2 | E69854 | hypothetical prote | 931 | 5 | 2.6 | 92 | 2 | S55663 | hypothetical prote |
| 859 | 2.6 | 79 | 2 | AE2014 | hypothetical prote | 932 | 5 | 2.6 | 93 | 2 | A97421 | PH adaptation pota |
| 860 | 2.6 | 80 | 2 | S60835 | M protein - curt | 933 | 5 | 2.6 | 93 | 2 | AH2638 | transcription regu |
| 861 | 2.6 | 80 | 2 | I39417 | epidermal growth f | 934 | 5 | 2.6 | 93 | 2 | AB3472 | phage related prot |
| 862 | 2.6 | 80 | 2 | I49469 | epidermal growth f | 935 | 5 | 2.6 | 93 | 2 | AB1729 | exo-alpha-sialidas |
| 863 | 2.6 | 80 | 2 | AC2394 | hypothetical prote | 936 | 5 | 2.6 | 94 | 2 | A00888 | histone-like prote |
| 864 | 2.6 | 80 | 2 | A12504 | hypothetical prote | 937 | 5 | 2.6 | 94 | 2 | D82712 | DNA binding protei |
| 865 | 2.6 | 81 | 2 | S22455 | hypothetical prote | 938 | 5 | 2.6 | 94 | 2 | AH2297 | virulence associat |
| 866 | 2.6 | 81 | 2 | A82251 | molybdenum cofacto | 939 | 5 | 2.6 | 94 | 2 | T09450 | virulence associat |
| 867 | 2.6 | 81 | 2 | E71523 | hypothetical prote | 940 | 5 | 2.6 | 94 | 2 | C64559 | M protein - curt |
| 868 | 2.6 | 82 | 1 | QFBO | micro glutamic aci | 941 | 5 | 2.6 | 94 | 2 | S60794 | papx protein - Esc |
| 869 | 2.6 | 82 | 2 | S61822 | M-like protein enn | 942 | 5 | 2.6 | 94 | 2 | T02230 | hypothetical prote |
| 870 | 2.6 | 82 | 2 | S71166 | RNA-directed DNA p | 943 | 5 | 2.6 | 94 | 2 | T28763 | transcription regu |
| 871 | 2.6 | 82 | 2 | A99836 | hypothetical prote | 944 | 5 | 2.6 | 94 | 2 | D84117 | Ig kappa chain V r |
| 872 | 2.6 | 82 | 2 | T41857 | AcMNPV orf120 - Bo | 945 | 5 | 2.6 | 95 | 2 | D37330 | acyl carrier prote |
| 873 | 2.6 | 82 | 2 | C85694 | unknown protein en | 946 | 5 | 2.6 | 95 | 2 | A47030 | probable sigma-54 |
| 874 | 2.6 | 83 | 2 | F71517 | probable L27 ribos | 947 | 5 | 2.6 | 95 | 2 | G82065 | hypothetical prote |
| 875 | 2.6 | 83 | 2 | E81673 | ribosomal protein | 948 | 5 | 2.6 | 95 | 2 | A82453 | hypothetical prote |
| 876 | 2.6 | 83 | 2 | A45466 | glycine/tyrosine-r | 949 | 5 | 2.6 | 95 | 2 | T46086 | hypothetical prote |
| 877 | 2.6 | 83 | 2 | H84098 | hypothetical prote | 950 | 5 | 2.6 | 95 | 2 | H97031 | hypothetical prote |
| 878 | 2.6 | 84 | 1 | TPPG | insulin precursor | 951 | 5 | 2.6 | 96 | 1 | CCQFF2 | cytochrome c2, iso |
| 879 | 2.6 | 84 | 2 | S06077 | H+-transporting tw | 952 | 5 | 2.6 | 96 | 1 | S49144 | amoebapore B precu |
| 880 | 2.6 | 84 | 2 | T24385 | hypothetical prote | 953 | 5 | 2.6 | 96 | 1 | MFIV2K | matrix protein M2 |
| 881 | 2.6 | 84 | 2 | A89984 | hypothetical prote | 954 | 5 | 2.6 | 96 | 1 | MFIV2F | matrix protein M2 |
| 882 | 2.6 | 85 | 2 | H82952 | atp synthase C cha | 955 | 5 | 2.6 | 96 | 1 | ZEBPG4 | gene B protein - p |
| 883 | 2.6 | 85 | 2 | H84728 | hypothetical prote | 956 | 5 | 2.6 | 96 | 2 | S11219 | nonhistone chromos |
| 884 | 2.6 | 85 | 2 | H69191 | hypothetical prote | 957 | 5 | 2.6 | 96 | 2 | S60842 | M protein - curt |
| 885 | 2.6 | 85 | 2 | T16045 | hypothetical prote | 958 | 5 | 2.6 | 96 | 2 | S61804 | M-like protein enn |
| 886 | 2.6 | 85 | 2 | S00071 | keratin high-tyros | 959 | 5 | 2.6 | 96 | 2 | R82311 | conserved hypothet |
| 887 | 2.6 | 86 | 1 | ZCBPF4 | gene C protein - p | 960 | 5 | 2.6 | 96 | 2 | A87110 | conserved hypothet |
| 888 | 2.6 | 86 | 2 | S07119 | ribulose-bisphosph | 961 | 5 | 2.6 | 96 | 2 | F64319 | hypothetical prote |
| 889 | 2.6 | 86 | 2 | S53701 | ribosomal protein | 962 | 5 | 2.6 | 96 | 2 | AB2692 | hypothetical prote |
| 890 | 2.6 | 86 | 2 | J50453 | gene C protein - p | 963 | 5 | 2.6 | 97 | 1 | CCQFM2 | cytochrome c2, iso |
| 891 | 2.6 | 86 | 2 | G90666 | probable DNA bindi | 964 | 5 | 2.6 | 97 | 1 | MMIV2 | matrix protein M2 |
| 892 | 2.6 | 86 | 2 | G85516 | probable ATP bindi | 965 | 5 | 2.6 | 97 | 1 | MFIV62 | matrix protein M2 |
| 893 | 2.6 | 86 | 2 | G90675 | probable ATP bindi | 966 | 5 | 2.6 | 97 | 1 | UN0393 | matrix protein M2 |
| 894 | 2.6 | 86 | 2 | D64016 | hypothetical prote | 967 | 5 | 2.6 | 97 | 1 | MFIV2M | matrix protein M2 |
| 895 | 2.6 | 86 | 2 | C97083 | uncharacterized pr | 968 | 5 | 2.6 | 97 | 1 | PN0084 | matrix protein M2 |
| 896 | 2.6 | 86 | 2 | B85526 | probable ATP bindi | 969 | 5 | 2.6 | 97 | 1 | C45539 | matrix protein M2 |
| 897 | 2.6 | 87 | 2 | S26282 | retrovirus-related | 970 | 5 | 2.6 | 97 | 2 | S18023 | matrix protein M2 |
| 898 | 2.6 | 87 | 2 | D95032 | conserved hypothet | 971 | 5 | 2.6 | 97 | 2 | S26341 | ribulose-bisphosph |
| 899 | 2.6 | 87 | 2 | D37903 | hypothetical prote | 972 | 5 | 2.6 | 97 | 2 | S36066 | Ig light chain V r |
| 900 | 2.6 | 88 | 2 | S03442 | class II histocomp | 973 | 5 | 2.6 | 97 | 2 | S61811 | Ig light chain V r |
| 901 | 2.6 | 88 | 2 | S60837 | M protein - curt | 974 | 5 | 2.6 | 97 | 2 | S04057 | M-like protein enn |
| 902 | 2.6 | 88 | 2 | H47759 | retrovirus-related | 975 | 5 | 2.6 | 97 | 2 | S04061 | matrix protein M2 |
| 903 | 2.6 | 88 | 2 | G42465 | hypothetical prote | 976 | 5 | 2.6 | 97 | 2 | S14617 | matrix protein M2 |
| 904 | 2.6 | 88 | 2 | JW0029 | hypothetical 9.7K | 977 | 5 | 2.6 | 97 | 2 | S04051 | matrix protein M2 |
| 905 | 2.6 | 88 | 2 | D91167 | hypothetical prote | 978 | 5 | 2.6 | 97 | 2 | | |

| | | | | | | |
|------|---|-----|-----|---|--------|--------------------------------|
| 979 | 5 | 2.6 | 97 | 2 | S28884 | ndhJ protein - soy |
| 980 | 5 | 2.6 | 97 | 2 | T03940 | hypothetical prote |
| 981 | 5 | 2.6 | 97 | 2 | D75277 | hypothetical prote |
| 982 | 5 | 2.6 | 97 | 2 | B81668 | conserved hypotet |
| 983 | 5 | 2.6 | 98 | 2 | S36062 | Ig lambda chain - |
| 984 | 5 | 2.6 | 98 | 2 | G64693 | hypothetical prote |
| 985 | 5 | 2.6 | 98 | 2 | D71807 | hypothetical prote |
| 986 | 5 | 2.6 | 98 | 2 | C75292 | hypothetical prote |
| 987 | 5 | 2.6 | 98 | 2 | H75494 | hypothetical prote |
| 988 | 5 | 2.6 | 98 | 2 | E43943 | lactococcin A immu |
| 989 | 5 | 2.6 | 98 | 2 | B33443 | lactococcin A immu |
| 990 | 5 | 2.6 | 98 | 2 | S36037 | FL-160 protein - T |
| 991 | 5 | 2.6 | 98 | 2 | AG2307 | hypothetical prote |
| 992 | 5 | 2.6 | 99 | 1 | CCQF2F | cytochrome c2, iso |
| 993 | 5 | 2.6 | 99 | 2 | I40317 | DNA repair protein |
| 994 | 5 | 2.6 | 99 | 2 | F98105 | conserved hypotet |
| 995 | 5 | 2.6 | 99 | 2 | T33486 | hypothetical prote |
| 996 | 5 | 2.6 | 99 | 2 | T32866 | hypothetical prote |
| 997 | 5 | 2.6 | 99 | 2 | G97228 | glu-tRNA ^{Gln} amidot |
| 998 | 5 | 2.6 | 99 | 2 | C98057 | hypothetical prote |
| 999 | 5 | 2.6 | 100 | 1 | CCQF2M | cytochrome c2, iso |
| 1000 | 5 | 2.6 | 100 | 1 | S26080 | ribosomal protein |

ALIGNMENTS

RESULT 1
 ADAD41
 L3 23K proteinase (EC 3.4.22.-) - human adenovirus 41
 Species: Mastadenovirus h41 (human adenovirus 41)
 Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
 Accession: E28645; S08658
 Authors: H.L.; van der Lee, F.M.; Remst, A.M.C.B.; van Loon, A.E.; Sussenbach, J.S.
 Title: The genes encoding the DNA binding protein and the 23K protease of adenovirus t
 Reference number: A94371; PMID:88160034; PMID:3279700
 Accession: E28645
 Molecule type: DNA
 Residues: 1-214 <VOS>
 Cross-references: GB:M21163; NID:G209865; PIDN:AAA2462.1; PID:G209869
 Toogood, C.I.A.; Murali, R.; Burnett, M.; Hay, R.T.
 Submitted to the EMBL Data Library, February 1990
 Reference number: S08656

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Query Match          4.1%; Score 8; DB 1; Length 214;
Best Local Similarity 100.0%; Pred.No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      YY      87 GCGSYFLG 94
      |||||
      bb      16 GCGSYFLG 23

RESULT 2
9996545
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Accession: E96545
Arabis:Theologis, A.; Becker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
T.H.; V. ; Yin, X.; Yin, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

```

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
A; Accession: B96545
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-528 <STO>
A; cross-references: GB:AE005173; NID:gl1094694; PIDN:AAG29630.1; GSPDB:GNC0141
C; Genetics:
A; Gene: F8A12.6
A; Map position: 1

| | | | | |
|-----------------------|---------|-----------------|---------------|-------------|
| Query Match | 4.1%; | Score 8; | DB 2; | Length 528; |
| Best Local Similarity | 100.0%; | Pred. No. 6; | | |
| Matches | 8; | Conservative 0; | Mismatches 0; | Indels 0; |
| QY | 6 | GFLVLWLS | 13 | |
| | | | | |
| | 189 | GFLVLWLS | 196 | |

RESULT 3
T39291
hypothetical CMH2 zinc finger protein - fission yeast (*Schizosaccharomyces pombe*)
C/Species: *Schizosaccharomyces pombe*
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T39291
R/McDonough, R.C.; Rajandream, M.A.; Barrell, B.G.; Ransperger, U.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, July 1999
A/Reference number: Z21841
A/Accession: T39291
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Crosses: 1-837 <MCD>
A/Cross-references: EMBL:AL096851; PIDN: CAB50977.1; GSPDB: GNO0067; SPDB: SPBC1105.14
A/Experimental source: strain 972h; cosmid c1105
C/Genetics:
A/Gene: SPDB: SPBC1105.14
A/Map position: 2

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Query Match          4.1%; Score 8; DB 2; Length 637;
Best Local Similarity 100.0%; Fred. No. 6.9; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy      142  SDLKRSLG 149
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Db       279  SDLKRSLG 286

RESULT 4
hypothetical protein P8A12.7 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96545
R:Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.;
ansen, N.P.; Hughes, B.; Huizar, L.

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C:Genetics:
A:Gene: F8A12.7
A:Map position: 1
Query Match
Best Local Similarity 4.1%; Score 8; DB 2; Length 768;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 FLVLWLSL 14
DB 214 FLVLWLSL 221
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|||||

RESULT 5
A:2413
Hypothetical protein asl4865 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: A12413
R:Kakazaki, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
R.; Kaneko, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12413
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA076564.1; PID:g17134002; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl4865
Query Match
Best Local Similarity 3.6%; Score 7; DB 2; Length 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 YFLGLKV 97
DB 54 YFLGLKV 60
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|||||

RESULT 6
C:90225
Hypothetical protein SSO6469 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: C90225
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813934; PIDN:AAK41058.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO6469
Query Match
Best Local Similarity 3.6%; Score 7; DB 2; Length 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 75 MPRPGYK 81
DB 1 MPRPGYK 7
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|||||

RESULT 7
C:90342
Hypothetical protein SSO8938 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: C90342
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90342
A:Status: preliminary
A:Molecule type: DNA
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C:Genetics:
A:Gene: SSO8938
Query Match
Best Local Similarity 3.6%; Score 7; DB 2; Length 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 75 MPRPGYK 81
DB 1 MPRPGYK 7
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|||||

RESULT 8
C:95Y1B
acidic ribosomal protein P2.e.a, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: acidic ribosomal protein A2; acidic ribosomal protein P2.beta; protein
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000
C:Accession: B28104; S00679; B35109; S66724; A49495
R:Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.
J. Biol. Chem. 263, 9094-9101, 1988
A:Title: Independent genes coding for three acidic proteins of the large ribosomal subuni
A:Reference number: A92726; MUID:88243786; PMID:2837476
A:Accession: B28104
A:Molecule type: DNA
A:Residues: 1-106 <REM>
A:Cross-references: EMBL:J03760; NID:g172395; PIDN:AAA34971.1; PID:g172396
R:Mitsui, K.; Tsurugi, K.
Nucleic Acids Res. 16, 3575, 1988
A:Title: cDNA and deduced amino acid sequence of acidic ribosomal protein A2 from Sacchar
A:Reference number: S00679; MUID:88233944; PMID:3287329
A:Accession: S00679
A:Molecule type: mRNA
A:Residues: 1-106 <MIT>
A:Cross-references: EMBL:X06958; NID:g4374; PIDN:CAA30028.1; PID:g4375
R:Newton, C.H.; Shimmin, L.C.; Yee, J.; Dennis, P.P.
J. Bacteriol. 172, 579-588, 1990
A:Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae ribo
1 protein.
A:Reference number: A35109; MUID:90130289; PMID:2404943
A:Accession: B35109
A:Molecule type: DNA
A:Residues: 1-106 <NEW>
A:Cross-references: GB:M26503; NID:g171816; PIDN:AAA34735.1; PID:g171817
R:Habbig, B.; Hattenhorst, U.; Hollenberg, C.P.; Ramezani Rad, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66703
A:Accession: S66722
A:Molecule type: DNA
A:Residues: 1-106 <HAB>
A:Cross-references: EMBL:Z74781; NID:gl419834; PIDN:CAA99041.1; PID:gl419835; GSPDB:GN000
R:Ansong, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wienann, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66723
A:Accession: S66724
A:Molecule type: DNA

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A;Residues: 1-106 <ANS>
A;Cross-references: EMBL:Z74781; NID:G1419834; PIDN:CAA99041.1; PID:G1419835; GSPDB:GN00
A;Experimental source: strain S28C
R;Santos, C.; Ortiz-Reyes, B.; Naranda, T.; Remacha, M.; Ballesta, J.P.G.
Biochemistry 32, 4231-4236, 1993
A;Title: The acidic phosphoproteins from Saccharomyces cerevisiae ribosomes. NH-2-termin
A;Reference number: A49495; MUID:93237229; PMID:8476850
A;Accession: A49495
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <SAN>
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A;Gene: SGD:RPLA2; RPA2; MIPS:YOL039W
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A;Map position: 15L
C;Superfamily: rat acidic ribosomal protein P1
C;Keywords: phosphoprotein; protein biosynthesis; ribosome

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
DB 84 ABEKEE 90

RESULT 9
R8BY2B
N;Alternate names: acidic ribosomal protein P1.e.B, cytosolic - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 21-Jul-2000
C;Accession: C28104; D35109; C49495; S67673
R;Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.
J. Biol. Chem. 263, 9094-9101, 1988
A;Title: Independent genes coding for three acidic proteins of the large ribosomal subun
A;Reference number: A92726; MUID:88243786; PMID:2837476
A;Accession: C28104
A;Molecule type: DNA
A;Residues: 1-106 <REM>
A;Cross-references: EMBL:M19238; NID:G172399; PIDN:AAA34973.1; PID:G172400
R;Newton, C.H.; Shimmin, L.C.; Yee, J.; Dennis, P.P.
J. Bacteriol. 172, 579-588, 1990
A;Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib
1 protein.
A;Reference number: A35109; MUID:90130289; PMID:2404943
A;Accession: D35109
A;Molecule type: DNA
A;Residues: 1-106 <NEW>
A;Cross-references: EMBL:M26507; NID:G171814; PIDN:AAA34734.1; PID:G171815
R;Santos, C.; Ortiz-Reyes, B.; Naranda, T.; Remacha, M.; Ballesta, J.P.G.
Biochemistry 32, 4231-4236, 1993
A;Title: The acidic phosphoproteins from Saccharomyces cerevisiae ribosomes. NH-2-termin
A;Reference number: A49495; MUID:93237229; PMID:8476850
A;Accession: C49495
A;Status: preliminary
A;Molecule type: protein
A;Residues: 9-16 <SAN>
A;Accession: B49495
A;Status: preliminary
A;Molecule type: protein
A;Residues: 2-5 <SAW>
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.; Wagner, G.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67655
A;Accession: S67673
A;Molecule type: DNA
A;Residues: 1-106 <RIB>
A;Cross-references: EMBL:Z74178; NID:G1431196; PIDN:CAA98698.1; PID:G1431197; GSPDB:GN00
A;Experimental source: strain S28C
C;Genetics:
A;Gene: SGD:RPLA3; RPL44; MIPS:YDL130W

A;Cross-references: SGD:S0002288; MIPS:YDL130W
A;Map position: 4L
A;Introns: 38/3
C;Superfamily: rat acidic ribosomal protein P1
C;Keywords: phosphoprotein; protein biosynthesis; ribosome

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
DB 84 ABEKEE 90

RESULT 10
T2147
ribosomal protein rpl1 [imported] - yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C;Accession: T52147
R;Taylor, K.; Harris, D.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z25985
A;Accession: T52147
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-106 <TAY>
A;Cross-references: EMBL:AL033497; PIDN:CAA21967.1
A;Experimental source: strain 1161; Cosmid Ca49C10
C;Genetics:
A;Gene: rpl1
A;Map position: 1
C;Superfamily: rat acidic ribosomal protein P1
C;Keywords: protein biosynthesis; ribosome

Query Match 3.6%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ABEKEE 193
DB 84 ABEKEE 90

RESULT 11
R5YV1
acidic ribosomal protein P2.e.B, cytosolic - yeast (Saccharomyces cerevisiae)
N;Alternate names: acidic ribosomal protein P2.alpha; protein D9481.1; protein YDR382W; 1
C;Species: Saccharomyces cerevisiae
C;Date: 31-Oct-1980 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C;Accession: A35109; A28104; A02776; S61177; S69666
R;Newton, C.H.; Shimmin, L.C.; Yee, J.; Dennis, P.P.
J. Bacteriol. 172, 579-588, 1990
A;Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib
1 protein.
A;Reference number: A35109; MUID:90130289; PMID:2404943
A;Accession: A35109
A;Molecule type: DNA
A;Residues: 1-110 <NEW>
A;Cross-references: GB:M26505; NID:G171810; PIDN:AAA34732.1; PID:G171811
R;Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.
J. Biol. Chem. 263, 9094-9101, 1988
A;Title: Independent genes coding for three acidic proteins of the large ribosomal subun
A;Reference number: A92726; MUID:88243786; PMID:2837476
A;Accession: A28104
A;Molecule type: DNA
A;Residues: 1-110 <REM>
A;Cross-references: EMBL:J03761; NID:G172397; PIDN:AAA34972.1; PID:G172398
A;Note: the authors translated the codon GAA for residue 28 as Ala
R;Itch, T.
Biochim. Biophys. Acta 671, 16-24, 1981
A;Title: Primary structure of an acidic ribosomal protein YPA1 from Saccharomyces cerevis

A;Residues: 1-298 <STE>
A;Cross-references: EMBL:U58743; PIDN:AAB0614.1; GSPDB:GN00028; CESP:F39F10.2
A;Experimental source: strain Bristol N2; clone F39F10

C:Genetics:
A:Gene: CESP:F39F10.2
A:Map position: X
A:Introns: 85/1; 146/3; 231/3
C:Superfamily: Kinase-related transforming protein; protein kinase homology

Query Match 3.6%; Score 7; DB 2; Length 298;
Best Local Similarity 100.0%; Fred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SLGGGLA 19
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Db 276 SLGGGLA 282

Search completed: May 17, 2004, 10:53:16
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 10:47:35 ; Search time 18 Seconds
(without alignments)
561.201 Million cell updates/sec

Title: US-10-621-401-145
Perfect score: 194
Sequence: 1 MKLASGFLVILWSLGGGLAQ.....PFMNSQRAACICABEKEEL 194

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 8 | 4.1 | 214 | 1 ADEN_ADE41 | P11826 human adeno |
| 4 | 7 | 3.6 | 106 | 1 RLA2 YEAST | P05319 saccharomyc |
| 5 | 7 | 3.6 | 106 | 1 RLA3 YEAST | P10622 saccharomyc |
| 6 | 7 | 3.6 | 110 | 1 RLA1 CLAEH | P50344 cladosporiu |
| 7 | 7 | 3.6 | 110 | 1 RLA4 YEAST | P02400 saccharomyc |
| 8 | 7 | 3.6 | 111 | 1 RLA4 CLAEH | P42039 cladosporiu |
| 9 | 7 | 3.6 | 204 | 1 TD53 HUMAN | Q16890 homo sapien |
| 10 | 7 | 3.6 | 204 | 1 TD53 MOUSE | Q54818 mus musculus |
| 11 | 7 | 3.6 | 210 | 1 TD53 CHICK | Q91864 gallus gall |
| 12 | 7 | 3.6 | 319 | 1 PA1 SERLI | P18952 serratia li |
| 13 | 7 | 3.6 | 338 | 1 RLA0 METJA | P54049 methanococc |
| 14 | 7 | 3.6 | 420 | 1 MSME STRMU | Q00749 streptococc |
| 15 | 7 | 3.6 | 434 | 1 CBPH BOVIN | P04836 bos taurus |
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| 17 | 7 | 3.6 | 476 | 1 CBPH MOUSE | Q00493 mus musculus |
| 18 | 7 | 3.6 | 476 | 1 CBPH RAT | P15087 rattus norv |
| 19 | 7 | 3.6 | 557 | 1 CAB1 AQJAE | Q67869 aquifex aeo |
| 20 | 7 | 3.6 | 585 | 1 SAC1 CHLRE | Q39593 chlamydomon |
| 21 | 7 | 3.6 | 649 | 1 S281 HUMAN | Q00337 homo sapien |
| 22 | 7 | 3.6 | 875 | 1 ARS2 MOUSE | Q99mr6 mus musculus |
| 23 | 7 | 3.6 | 875 | 1 ARS2 HUMAN | Q9bpx5 homo sapien |
| 24 | 7 | 3.6 | 1083 | 1 MAN1 YEAST | P22855 saccharomyc |
| 25 | 7 | 3.6 | 1135 | 1 RPC2 DROME | P25167 drosophila |
| 26 | 7 | 3.6 | 1191 | 1 SMC3 RAT | P97690 rattus norv |
| 27 | 7 | 3.6 | 1217 | 1 SMC3 HUMAN | Q9uq77 homo sapien |
| 28 | 7 | 3.6 | 1217 | 1 SMC3 MOUSE | Q9cwo3 mus musculus |
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| 31 | 7 | 3.6 | 4725 | 1 DYHC DICDI | P34036 dictyosteli |
| 32 | 6 | 3.1 | 68 | 1 YN40 THETN | Q9r7q8 thermoanaer |
| 33 | 6 | 3.1 | 70 | 1 UBIL_CABER | Q07371 caenorhabdi |

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| 35 | 6 | 3.1 | 74 | 1 Y350 METKA | Q8tyf0 methanopyru |
| 36 | 6 | 3.1 | 89 | 1 BAF HUMAN | Q75531 homo sapien |
| 37 | 6 | 3.1 | 89 | 1 BAF_MOUSE | Q54962 mus musculu |
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| 39 | 6 | 3.1 | 100 | 1 NUOK BUCBP | Q89at7 buchnera ap |
| 40 | 6 | 3.1 | 102 | 1 LE19 GOSHI | P09443 gossypium h |
| 41 | 6 | 3.1 | 107 | 1 RL12 PYRAB | Q9uxs6 pyrococcus |
| 42 | 6 | 3.1 | 108 | 1 HX8 RAT | P18866 rattus norv |
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| 44 | 6 | 3.1 | 110 | 1 RL21 ALTAL | P49148 alternaria |
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| 46 | 6 | 3.1 | 111 | 1 RL23 ASPFU | Q9uuz6 aspergillus |
| 47 | 6 | 3.1 | 111 | 1 RLA3 CLAEH | P42038 cladosporiu |
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| 50 | 6 | 3.1 | 115 | 1 RK20 CYACA | Q9tl80 cyanidium c |
| 51 | 6 | 3.1 | 119 | 1 RLA3 MAIZE | Q24413 zea mays (m |
| 52 | 6 | 3.1 | 122 | 1 YU2C BACSU | Q32089 bacillus su |
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| 54 | 6 | 3.1 | 128 | 1 Y280 METJA | Q57728 methanococc |
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| 57 | 6 | 3.1 | 167 | 1 YDAE BACSU | P96578 bacillus su |
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| 59 | 6 | 3.1 | 171 | 1 GCS4 AQUAE | Q67192 aquifex aeo |
| 60 | 6 | 3.1 | 173 | 1 NUGM GADMO | P55783 gadus morhu |
| 61 | 6 | 3.1 | 176 | 1 AROK MYCTU | P95014 mycobacteri |
| 62 | 6 | 3.1 | 182 | 1 MCRC METVO | P11567 methanococc |
| 63 | 6 | 3.1 | 186 | 1 FRBQ DROME | P37236 drosophila |
| 64 | 6 | 3.1 | 189 | 1 PA2Y HUMAN | Q9b2m1 homo sapien |
| 65 | 6 | 3.1 | 191 | 1 RNMC MONCH | P23540 momordica c |
| 66 | 6 | 3.1 | 192 | 1 PA2V MOUSE | Q9ep22 mus musculu |
| 67 | 6 | 3.1 | 196 | 1 IF3 WIGHR | Q8d3b9 wigleswort |
| 68 | 6 | 3.1 | 198 | 1 MCRC METVA | P07960 methanococc |
| 69 | 6 | 3.1 | 200 | 1 MCRC METJA | Q58254 methanococc |
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| 71 | 6 | 3.1 | 203 | 1 RUVA ECOLI | P08576 escherichia |
| 72 | 6 | 3.1 | 203 | 1 RUVA SALTY | Q8xth9 salmonella |
| 73 | 6 | 3.1 | 204 | 1 RUVA YERPE | Q8zeu6 versinia pe |
| 74 | 6 | 3.1 | 205 | 1 RUVA PSEPK | Q88j11 pseudomonas |
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| 76 | 6 | 3.1 | 211 | 1 RCN1 YEAST | P36054 saccharomyc |
| 77 | 6 | 3.1 | 213 | 1 NEUM CARAU | P17691 carassius a |
| 78 | 6 | 3.1 | 221 | 1 CFI PHAVU | P14238 phaseolus v |
| 79 | 6 | 3.1 | 222 | 1 ERF4 ARATH | Q80340 arabidopsis |
| 80 | 6 | 3.1 | 224 | 1 CFI FUELO | Q43056 pueraria lo |
| 81 | 6 | 3.1 | 226 | 1 NEUM RAT | P07936 rattus norv |
| 82 | 6 | 3.1 | 228 | 1 NEUA HAEIN | Q57140 haemophilus |
| 83 | 6 | 3.1 | 232 | 1 PSD RHILLO | Q984w0 rhizobium l |
| 84 | 6 | 3.1 | 232 | 1 YK10 ARCFU | Q28269 archaeoglob |
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| 86 | 6 | 3.1 | 239 | 1 3MGH PSEAE | Q9hx17 pseudomonas |
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| 88 | 6 | 3.1 | 239 | 1 GIDB CLOTE | Q89980 clostridium |
| 89 | 6 | 3.1 | 242 | 1 HXC8 HUMAN | P31273 homo sapien |
| 90 | 6 | 3.1 | 242 | 1 HXC8 MOUSE | P09025 mus musculu |
| 91 | 6 | 3.1 | 243 | 1 TRMD BACSU | Q31741 bacillus su |
| 92 | 6 | 3.1 | 247 | 1 AXID ARATH | Q38831 arabidopsis |
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| 96 | 6 | 3.1 | 259 | 1 YG47 SYNY3 | P74369 synechocyst |
| 97 | 6 | 3.1 | 260 | 1 TH14 METAC | Q8tm19 methanosaar |
| 98 | 6 | 3.1 | 260 | 1 TH14 METJA | Q8q0b5 methanosaar |
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| 101 | 6 | 3.1 | 280 | 1 THTM ECO57 | P58388 escherichia |
| 102 | 6 | 3.1 | 280 | 1 THTM ECOLI | P31142 escherichia |
| 103 | 6 | 3.1 | 281 | 1 RP32 HAEIN | P44404 haemophilus |
| 104 | 6 | 3.1 | 282 | 1 VFHH ECOLI | P37767 escherichia |
| 105 | 6 | 3.1 | 283 | 1 BRUI SOYBN | P35694 glycine max |
| 106 | 6 | 3.1 | 284 | 1 DAPF_BUCAI | P57649 buchnera ap |

| | | | | | | | | | | | | | | | |
|-----|---|-----|-----|---|------------|--------|--------------|-----|---|-----|-----|---|------------|--------|-------------|
| 107 | 6 | 3.1 | 284 | 1 | POLG_PVYVO | P11897 | potato viru | 180 | 6 | 3.1 | 421 | 1 | EXOF_RHIME | Q02728 | thizobium m |
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| 109 | 6 | 3.1 | 285 | 1 | RP32_ENTCL | P50508 | enterobacte | 182 | 6 | 3.1 | 421 | 1 | SYH_CORSU | Q83C80 | coxiella bu |
| 110 | 6 | 3.1 | 289 | 1 | XL15_ARATH | Q38911 | arabidopsis | 183 | 6 | 3.1 | 422 | 1 | PAN1_HUMAN | Q14653 | homo sapien |
| 111 | 6 | 3.1 | 290 | 1 | ILVE_RICCN | Q92126 | rickettsia | 184 | 6 | 3.1 | 427 | 1 | IRF3_HUMAN | Q14653 | homo sapien |
| 112 | 6 | 3.1 | 290 | 1 | ILVE_RICPR | O05970 | rickettsia | 185 | 6 | 3.1 | 427 | 1 | YF05_MEITH | O27549 | methanobact |
| 113 | 6 | 3.1 | 291 | 1 | CHIA_TOBAC | O29060 | nicotiana t | 186 | 6 | 3.1 | 427 | 1 | YK15_YEAST | P36046 | saccharomyc |
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| 115 | 6 | 3.1 | 293 | 1 | CHIA_CICAR | P36908 | cicer ariet | 188 | 6 | 3.1 | 429 | 1 | PUR2_SALTI | Q8z334 | salmonella |
| 116 | 6 | 3.1 | 293 | 1 | ACTR_SHEEP | Q9tu77 | ovis aries | 189 | 6 | 3.1 | 429 | 1 | PUR2_SALTY | P26977 | salmonella |
| 117 | 6 | 3.1 | 296 | 1 | ACTR_MOUSE | Q64326 | mus musculu | 190 | 6 | 3.1 | 430 | 1 | MURD_THEMA | Q8wy76 | thermotoga |
| 118 | 6 | 3.1 | 296 | 1 | VG21_HSV11 | Q00114 | ictaluriid h | 191 | 6 | 3.1 | 430 | 1 | TOLB_YERPE | Q8zgz1 | yersinia pe |
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| 120 | 6 | 3.1 | 298 | 1 | REM_HUMAN | O75628 | homo sapien | 193 | 6 | 3.1 | 433 | 1 | KKQ1_YEAST | P36005 | saccharomyc |
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| 122 | 6 | 3.1 | 310 | 1 | KITH_HSVTF | P31577 | turkey herp | 195 | 6 | 3.1 | 434 | 1 | SYH_BORPE | Q7w6p7 | bordetella |
| 123 | 6 | 3.1 | 311 | 1 | CHLY_HEVER | P23472 | hevea bras | 196 | 6 | 3.1 | 437 | 1 | RBL1_ARCFU | Q28685 | archaeoglob |
| 124 | 6 | 3.1 | 313 | 1 | RLA0_NEUCR | Q96tj5 | neurospora | 197 | 6 | 3.1 | 438 | 1 | ARP6_YEAST | Q12509 | saccharomyc |
| 125 | 6 | 3.1 | 320 | 1 | Y678_METJA | P53156 | saccharomyc | 198 | 6 | 3.1 | 440 | 1 | PPAS_MOUSE | P35396 | mus musculu |
| 126 | 6 | 3.1 | 320 | 1 | Y678_METJA | Q89gnl | homo sapien | 199 | 6 | 3.1 | 441 | 1 | PPAS_MOUSE | Q03181 | homo sapien |
| 127 | 6 | 3.1 | 323 | 1 | HEM2_SYNY3 | P77969 | synecocyst | 200 | 6 | 3.1 | 442 | 1 | G6PI_MYCSM | P96803 | mycobacteri |
| 128 | 6 | 3.1 | 327 | 1 | HEM2_SYNY3 | O67876 | aquifex aeo | 201 | 6 | 3.1 | 445 | 1 | GLNA_LACDE | P45627 | lactobacill |
| 129 | 6 | 3.1 | 330 | 1 | RS2_MYCPU | Q98g36 | mycoplasma | 202 | 6 | 3.1 | 445 | 1 | THB1_COLGR | P22013 | colletotric |
| 130 | 6 | 3.1 | 330 | 1 | RS2_MYCPU | Q98g36 | mycoplasma | 203 | 6 | 3.1 | 446 | 1 | NY5R_CANFA | O62729 | canis famli |
| 131 | 6 | 3.1 | 331 | 1 | GNTR_ECOLI | P46860 | escherichia | 204 | 6 | 3.1 | 446 | 1 | NY5R_PIG | O97969 | sus scrofa |
| 132 | 6 | 3.1 | 332 | 1 | PASA_HUMAN | O8izul | homo sapien | 205 | 6 | 3.1 | 448 | 1 | PRTE_BACNO | P19577 | bacteroides |
| 133 | 6 | 3.1 | 334 | 1 | CATL_PIG | Q28944 | homo sapien | 206 | 6 | 3.1 | 455 | 1 | NY5R_HUMAN | Q15761 | homo sapien |
| 134 | 6 | 3.1 | 335 | 1 | HEM2_METJA | Q60178 | methanococc | 207 | 6 | 3.1 | 456 | 1 | NY5R_RAT | Q63634 | rattus norv |
| 135 | 6 | 3.1 | 337 | 1 | HNR_ECOLI | P37055 | escherichia | 208 | 6 | 3.1 | 460 | 1 | PTSB_BACSU | P05306 | bacillus su |
| 136 | 6 | 3.1 | 338 | 1 | RLA0_METTL | O52705 | methanococc | 209 | 6 | 3.1 | 460 | 1 | YDDV_ECOLI | P77793 | escherichia |
| 137 | 6 | 3.1 | 339 | 1 | RLA0_ARCTU | O28781 | archaeoglob | 210 | 6 | 3.1 | 462 | 1 | SYN_SYNY3 | P52276 | synecocyst |
| 138 | 6 | 3.1 | 340 | 1 | Y231_LISMO | Q49759 | listeria mo | 211 | 6 | 3.1 | 465 | 1 | GLGA_SYN7 | Q935Y7 | synecococc |
| 139 | 6 | 3.1 | 340 | 1 | Y263_LISIN | Q92f44 | listeria in | 212 | 6 | 3.1 | 466 | 1 | CMGA_RAT | P10354 | rattus norv |
| 140 | 6 | 3.1 | 341 | 1 | CYTR_ECOLI | P06964 | escherichia | 213 | 6 | 3.1 | 466 | 1 | NY5R_MOUSE | O70342 | mus musculu |
| 141 | 6 | 3.1 | 342 | 1 | PYRC_SYNY3 | P74438 | synecocyst | 214 | 6 | 3.1 | 470 | 1 | MM12_HUMAN | P39900 | homo sapien |
| 142 | 6 | 3.1 | 342 | 1 | RLA0_PRRHO | O74109 | pyrococcus | 215 | 6 | 3.1 | 471 | 1 | TIG_ANASP | Q8YqX9 | anabaena sp |
| 143 | 6 | 3.1 | 346 | 1 | GATD_ECOLI | P37190 | escherichia | 216 | 6 | 3.1 | 477 | 1 | MM03_HORSE | Q28397 | equus cabal |
| 144 | 6 | 3.1 | 348 | 1 | LPXD_BARHE | O8vg23 | bartonella | 217 | 6 | 3.1 | 480 | 1 | HDA1_CHICK | P56517 | gallus gall |
| 145 | 6 | 3.1 | 349 | 1 | ARSA_METJA | Q58542 | methanococc | 218 | 6 | 3.1 | 484 | 1 | MPPA_YEAST | P11914 | saccharomyc |
| 146 | 6 | 3.1 | 350 | 1 | KITH_HSVTU | P25987 | turkey herp | 219 | 6 | 3.1 | 484 | 1 | SLT2_YEAST | Q00772 | saccharomyc |
| 147 | 6 | 3.1 | 352 | 1 | ADD_LACLA | O9c1r9 | lactococcus | 220 | 6 | 3.1 | 485 | 1 | VST2_HEVRH | Q00270 | hepatitis e |
| 148 | 6 | 3.1 | 354 | 1 | AROB_SULSO | Q98019 | sulfolobus | 221 | 6 | 3.1 | 492 | 1 | SECY_CYAPA | P25014 | cyanophora |
| 149 | 6 | 3.1 | 355 | 1 | ATNE_PIG | Q9bdk6 | sus scrofa | 222 | 6 | 3.1 | 492 | 1 | TYTR_TRYBB | P39051 | trypanosoma |
| 150 | 6 | 3.1 | 357 | 1 | ATNE_PIG | Q9un42 | homo sapien | 223 | 6 | 3.1 | 492 | 1 | TYTR_TRYBB | P28593 | trypanosoma |
| 151 | 6 | 3.1 | 360 | 1 | CYS2_MAIZE | O10717 | zea mays | 224 | 6 | 3.1 | 494 | 1 | HMBC_DROME | P03081 | drosophila |
| 152 | 6 | 3.1 | 361 | 1 | APEA_DICDI | P51173 | dictyosteli | 225 | 6 | 3.1 | 494 | 1 | SYE_PSEAE | Q9xc16 | pseudomonas |
| 153 | 6 | 3.1 | 361 | 1 | AROB_SYNY3 | P73997 | synecocyst | 226 | 6 | 3.1 | 500 | 1 | XVNB_THESA | P36906 | thermoanaer |
| 154 | 6 | 3.1 | 361 | 1 | DCAM_DAUCA | Q9axe3 | daucus caro | 227 | 6 | 3.1 | 500 | 1 | XVNB_THESJ | Q03060 | thermoanaer |
| 155 | 6 | 3.1 | 362 | 1 | ALBU_HORVU | P05167 | hordeum vul | 228 | 6 | 3.1 | 501 | 1 | MKCI_CANAL | P43068 | candida alb |
| 156 | 6 | 3.1 | 362 | 1 | DCAM_DATST | Q96555 | datura stra | 229 | 6 | 3.1 | 501 | 1 | PLI3_ARATH | Q93204 | arabidopsis |
| 157 | 6 | 3.1 | 363 | 1 | ENGC_XANAC | Q89pw9 | xanthomonas | 230 | 6 | 3.1 | 502 | 1 | C718_MENPI | Q42716 | mentha pipe |
| 158 | 6 | 3.1 | 371 | 1 | PAGE_MOUSE | Q9jR83 | mus musculu | 231 | 6 | 3.1 | 502 | 1 | HXK2_ARATH | P93834 | arabidopsis |
| 159 | 6 | 3.1 | 372 | 1 | PAGE_MOUSE | Q9by95 | homo sapien | 232 | 6 | 3.1 | 503 | 1 | LCYB_NARPS | Q40424 | narcissus p |
| 160 | 6 | 3.1 | 376 | 1 | MED7_SCHPO | O50368 | schizosacch | 233 | 6 | 3.1 | 504 | 1 | FLIC_SALMO | Q08973 | salmonella |
| 161 | 6 | 3.1 | 376 | 1 | P33_MYCPE | O60104 | mycoplasma | 234 | 6 | 3.1 | 507 | 1 | FLIC_SALBE | Q08968 | salmonella |
| 162 | 6 | 3.1 | 380 | 1 | LE22_PYRAB | Q9v4j0 | pyrococcus | 235 | 6 | 3.1 | 507 | 1 | FLIC_SALBE | Q06974 | salmonella |
| 163 | 6 | 3.1 | 384 | 1 | PRTK_TRIAL | P06873 | tritirachiu | 236 | 6 | 3.1 | 511 | 1 | TRPE_STRCO | Q924W7 | streptomyce |
| 164 | 6 | 3.1 | 388 | 1 | RIMI_TRIAL | Q99ne5 | mus musculu | 237 | 6 | 3.1 | 512 | 1 | GUAA_THETN | Q8rc63 | thermoanaer |
| 165 | 6 | 3.1 | 390 | 1 | ARGD_METHH | O27392 | methanobact | 238 | 6 | 3.1 | 514 | 1 | CP24_HUMAN | Q07973 | homo sapien |
| 166 | 6 | 3.1 | 394 | 1 | CEGT_HUMAN | Q16739 | homo sapien | 239 | 6 | 3.1 | 514 | 1 | SYB_METMP | O30520 | methanococc |
| 167 | 6 | 3.1 | 395 | 1 | CRTC_CAEOL | P27798 | caenorhabdi | 240 | 6 | 3.1 | 523 | 1 | PUR9_STRCO | Q9ky50 | s bifunctio |
| 168 | 6 | 3.1 | 399 | 1 | PNCB_ECO57 | Q8x8e8 | escherichia | 241 | 6 | 3.1 | 524 | 1 | TXN2_HUMAN | Q9nmw7 | homo sapien |
| 169 | 6 | 3.1 | 399 | 1 | PNCB_ECOLI | P18133 | escherichia | 242 | 6 | 3.1 | 525 | 1 | WVIN_VIBCH | O34238 | vibrio chol |
| 170 | 6 | 3.1 | 403 | 1 | SYH_AQUAE | Q66522 | aquifex aeo | 243 | 6 | 3.1 | 529 | 1 | VGLF_SV5 | P04849 | simian viru |
| 171 | 6 | 3.1 | 406 | 1 | PKD3_HUMAN | Q15120 | homo sapien | 244 | 6 | 3.1 | 530 | 1 | NLFA_MOUSE | Q8bg30 | mus musculu |
| 172 | 6 | 3.1 | 412 | 1 | TGF3_CHICK | P16047 | gallus gall | 245 | 6 | 3.1 | 536 | 1 | THIP_ECOLI | Q16610 | homo sapien |
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| 174 | 6 | 3.1 | 414 | 1 | YOJL_BACSU | Q31852 | bacillus su | 247 | 6 | 3.1 | 541 | 1 | THS3_MOUSE | Q8k2w9 | mus musculu |
| 175 | 6 | 3.1 | 416 | 1 | PGK_AGRAB | O94123 | agarius bi | 248 | 6 | 3.1 | 548 | 1 | THS3_MOUSE | Q9va66 | aeropyrum p |
| 176 | 6 | 3.1 | 417 | 1 | PGK_ASPOR | P41756 | aspergillus | 249 | 6 | 3.1 | 549 | 1 | NLFA_HUMAN | Q9h3p2 | homo sapien |
| 177 | 6 | 3.1 | 418 | 1 | EF1G_ORYSA | Q9zri7 | oryza sativ | 250 | 6 | 3.1 | 552 | 1 | YHN8_YEAST | P38799 | saccharomyc |
| 178 | 6 | 3.1 | 419 | 1 | CMLA_PSEAE | P32482 | pseudomonas | 251 | 6 | 3.1 | 555 | 1 | NFL_COTJA | Q02916 | coturnix co |
| 179 | 6 | 3.1 | 420 | 1 | PR11_HUMAN | P49642 | homo sapien | 252 | 6 | 3.1 | 556 | 1 | HIR3_HUMAN | Q9bw71 | homo sapien |

| | | | | | | | | | | | | | |
|-----|---|-------------|-----|-----|---|-----|---|---------------------|-----|------|---|------------|---------------------|
| 253 | 1 | PAP CANAL | 558 | 3.1 | 6 | 3.1 | 1 | Q42617 candida alb | 326 | 798 | 1 | FBL1 CAEL | 077469 caenorhabdi |
| 254 | 1 | SYR MEETH | 560 | 3.1 | 6 | 3.1 | 1 | Q27496 methanobact | 327 | 805 | 1 | IF2 AQUAE | 067825 aquifex aeo |
| 255 | 1 | FLAJ METJA | 562 | 3.1 | 6 | 3.1 | 1 | Q58311 methanococ | 328 | 811 | 1 | SYQ SCHPO | Q9Y7Y8 schizosacch |
| 256 | 1 | SYP BUCAI | 572 | 3.1 | 6 | 3.1 | 1 | P57333 buchnera ap | 329 | 841 | 1 | IE63 MCMVS | Q69154 murine cyto |
| 257 | 1 | NUSM LUMTE | 574 | 3.1 | 6 | 3.1 | 1 | Q34947 lumbricus t | 330 | 855 | 1 | RDLS ARATH | Q8W3J8 arabidopsis |
| 258 | 1 | NODU RHTR | 575 | 3.1 | 6 | 3.1 | 1 | Q53515 rhizobium t | 331 | 857 | 1 | NFM CHICK | P16053 gallus gall |
| 259 | 1 | YL71 CAEL | 577 | 3.1 | 6 | 3.1 | 1 | Q20624 caenorhabdi | 332 | 860 | 1 | CHI2 COCPO | P54197 coccidioid |
| 260 | 1 | RHLE BRWCH | 578 | 3.1 | 6 | 3.1 | 1 | Q8rjp2 erwinia chr | 333 | 866 | 1 | LOX2 PEA | P14856 pisum sativ |
| 261 | 1 | CHT2 CANAL | 580 | 3.1 | 6 | 3.1 | 1 | Q40953 candida alb | 334 | 866 | 1 | MYSP SCHJA | Q05870 schistosoma |
| 262 | 1 | K2C5 HUMAN | 593 | 3.1 | 6 | 3.1 | 1 | P13847 homo sapien | 335 | 875 | 1 | MYSP SCHWA | Q06198 schistosoma |
| 263 | 1 | DSDI PSEAE | 591 | 3.1 | 6 | 3.1 | 1 | Q9huw5 pseudomonas | 336 | 881 | 1 | UBP7 SCHPO | Q09765 schizosacch |
| 264 | 1 | CALX HUMAN | 592 | 3.1 | 6 | 3.1 | 1 | P27824 homo sapien | 337 | 882 | 1 | DIS1 SCHPO | Q09933 schizosacch |
| 265 | 1 | NTP4 TOXGO | 592 | 3.1 | 6 | 3.1 | 1 | P52913 toxoplasma | 338 | 882 | 1 | RA50 PYRPU | P58301 pyrococcus |
| 266 | 1 | CALX CANFA | 593 | 3.1 | 6 | 3.1 | 1 | P24643 canis famil | 339 | 885 | 1 | RPA1 THEAC | Q03585 thermoplas |
| 267 | 1 | SYR CAUCR | 600 | 3.1 | 6 | 3.1 | 1 | Q9a347 caulobacter | 340 | 894 | 1 | WPA1 BACSU | P54423 bacillus su |
| 268 | 1 | RFAL DROME | 603 | 3.1 | 6 | 3.1 | 1 | Q24492 drosophila | 341 | 897 | 1 | SAP1 YEAST | P39955 saccharomyc |
| 269 | 1 | GLMS LEFIN | 609 | 3.1 | 6 | 3.1 | 1 | Q8ezq1 l glucosami | 342 | 901 | 1 | ACON STAAM | Q99uc8 staphylococ |
| 270 | 1 | YG4R YEAST | 613 | 3.1 | 6 | 3.1 | 1 | P50080 saccharomyc | 343 | 901 | 1 | ACON STAEP | Q8cp22 staphylococ |
| 271 | 1 | BTUB ECOLI | 614 | 3.1 | 6 | 3.1 | 1 | Q06129 escherichia | 344 | 908 | 1 | ACON BACSU | P09339 bacillus su |
| 272 | 1 | BTUB SALTY | 614 | 3.1 | 6 | 3.1 | 1 | P37409 salmonella | 345 | 908 | 1 | DPO1 BORBU | O51498 borrelia bu |
| 273 | 1 | YKRA YEAST | 618 | 3.1 | 6 | 3.1 | 1 | P36029 saccharomyc | 346 | 912 | 1 | PGCB BOVIN | Q28062 bos taurus |
| 274 | 1 | LCPI MOUSE | 619 | 3.1 | 6 | 3.1 | 1 | Q8bull1 mus musculu | 347 | 947 | 1 | PODK MAIZE | P11155 zea mays (m |
| 275 | 1 | LCPI RAT | 621 | 3.1 | 6 | 3.1 | 1 | Q99pm1 rattus norv | 348 | 947 | 1 | AHM6 ARATH | Q98a29 arabidopsis |
| 276 | 1 | LCPI HUMAN | 621 | 3.1 | 6 | 3.1 | 1 | Q94842 homo sapien | 349 | 950 | 1 | GYP2 YEAST | P53358 saccharomyc |
| 277 | 1 | YCXB PORPU | 621 | 3.1 | 6 | 3.1 | 1 | P51234 porphyra pu | 350 | 954 | 1 | K6P1 YARLI | P59680 yarrowia li |
| 278 | 1 | S6AB MOUSE | 627 | 3.1 | 6 | 3.1 | 1 | P31650 mus musculu | 351 | 970 | 1 | AND1 MOUSE | P59328 mus musculu |
| 279 | 1 | S6AB RAT | 627 | 3.1 | 6 | 3.1 | 1 | P31647 rattus norv | 352 | 974 | 1 | PODJ CAUCR | Q92988 caulobacter |
| 280 | 1 | SYR FYRPU | 629 | 3.1 | 6 | 3.1 | 1 | Q8u149 pyrococcus | 353 | 974 | 1 | VIL4 ARATH | O65570 arabidopsis |
| 281 | 1 | S6AB HUMAN | 632 | 3.1 | 6 | 3.1 | 1 | F48066 homo sapien | 354 | 974 | 1 | UB37 HUMAN | Q86582 homo sapien |
| 282 | 1 | SL56 RAT | 634 | 3.1 | 6 | 3.1 | 1 | Q70247 rattus norv | 355 | 979 | 1 | NPH1 ARATH | C48963 arabidopsis |
| 283 | 1 | NAF1 HUMAN | 636 | 3.1 | 6 | 3.1 | 1 | Q15025 homo sapien | 356 | 1003 | 1 | SYG CHLMU | Q9pic6 chlamydia m |
| 284 | 1 | YI19 MYCTU | 639 | 3.1 | 6 | 3.1 | 1 | Q50614 mycobacteri | 357 | 1003 | 1 | SYG CHLTR | O46371 chlamydia t |
| 285 | 1 | NFM EABIT | 644 | 3.1 | 6 | 3.1 | 1 | P54938 myctolagrus | 358 | 1016 | 1 | DPO1 RHILE | Q9s1g2 rhizobium l |
| 286 | 1 | ARH7 HUMAN | 646 | 3.1 | 6 | 3.1 | 1 | Q14155 homo sapien | 359 | 1017 | 1 | EM11 MOUSE | Q99k41 mus musculu |
| 287 | 1 | ARH7 RAT | 646 | 3.1 | 6 | 3.1 | 1 | Q55043 rattus norv | 360 | 1021 | 1 | SECA ARATH | Q98y10 arabidopsis |
| 288 | 1 | NAF1 MOUSE | 647 | 3.1 | 6 | 3.1 | 1 | Q9uuu8 mus musculu | 361 | 1025 | 1 | MK21 YEAST | Q12176 saccharomyc |
| 289 | 1 | SYM STAAM | 657 | 3.1 | 6 | 3.1 | 1 | Q99wb3 staphylococ | 362 | 1031 | 1 | YDG9 SCHPO | Q10496 schizosacch |
| 290 | 1 | SYM STAAM | 657 | 3.1 | 6 | 3.1 | 1 | Q8ny00 staphylococ | 363 | 1036 | 1 | SECA SPIOL | Q36795 spinacia ol |
| 291 | 1 | VST2 HEVME | 659 | 3.1 | 6 | 3.1 | 1 | Q03500 hepatitis e | 364 | 1048 | 1 | P100 HCMVA | P08318 human cytom |
| 292 | 1 | VST2 HEVBU | 660 | 3.1 | 6 | 3.1 | 1 | P29326 hepatitis e | 365 | 1049 | 1 | RD16 ARATH | Q94hw3 arabidopsis |
| 293 | 1 | VST2 HEVMA | 660 | 3.1 | 6 | 3.1 | 1 | Q04611 hepatitis e | 366 | 1051 | 1 | ULK1 MOUSE | Q70405 mus musculu |
| 294 | 1 | VST2 HEVPA | 666 | 3.1 | 6 | 3.1 | 1 | P33426 hepatitis e | 367 | 1059 | 1 | POL2 DROME | P20825 drosophila |
| 295 | 1 | PD14 RAT | 666 | 3.1 | 6 | 3.1 | 1 | Q88807 rattus norv | 368 | 1065 | 1 | DP3A STAEP | Q8cux0 staphylococ |
| 296 | 1 | RPOC MBVH | 668 | 3.1 | 6 | 3.1 | 1 | Q9mu66 mesostigma | 369 | 1066 | 1 | AOSL PLEHO | O16025 plexaura ho |
| 297 | 1 | RPOC ARATH | 681 | 3.1 | 6 | 3.1 | 1 | P56763 arabidopsis | 370 | 1073 | 1 | MTR4 YEAST | P47047 saccharomyc |
| 298 | 1 | RPOC SINHAL | 688 | 3.1 | 6 | 3.1 | 1 | P46819 sinapis alb | 371 | 1083 | 1 | KCH3 HUMAN | Q9uld8 homo sapien |
| 299 | 1 | ARKB PSEAE | 690 | 3.1 | 6 | 3.1 | 1 | P57698 pseudomonas | 372 | 1087 | 1 | KCH3 MOUSE | Q9wv10 mus musculu |
| 300 | 1 | ARKB PSEAE | 705 | 3.1 | 6 | 3.1 | 1 | Q9es28 mus musculu | 373 | 1087 | 1 | KCH3 RAT | O89047 rattus norv |
| 301 | 1 | RPSD MYXXA | 708 | 3.1 | 6 | 3.1 | 1 | P17531 myxococcus | 374 | 1112 | 1 | RA13 SCHPO | P28706 schizosacch |
| 302 | 1 | FTSI NEPOL | 709 | 3.1 | 6 | 3.1 | 1 | Q9tl136 nephroselmi | 375 | 1112 | 1 | TERT HUMAN | O14746 homo sapien |
| 303 | 1 | HS9A CHICK | 728 | 3.1 | 6 | 3.1 | 1 | P11501 gallus gall | 376 | 1132 | 1 | S126 HUMAN | Q9uhw9 homo sapien |
| 304 | 1 | NPH1 HUMAN | 732 | 3.1 | 6 | 3.1 | 1 | O15259 homo sapien | 377 | 1150 | 1 | S126 MOUSE | Q924n4 mus musculu |
| 305 | 1 | MK10 YEAST | 733 | 3.1 | 6 | 3.1 | 1 | Q02197 saccharomyc | 378 | 1150 | 1 | DNBI HSVB2 | P12639 bovine herp |
| 306 | 1 | AD02 MACFA | 735 | 3.1 | 6 | 3.1 | 1 | Q28478 macaca fasc | 379 | 1186 | 1 | KZ DROME | O46072 drosophila |
| 307 | 1 | DHB4 MOUSE | 735 | 3.1 | 6 | 3.1 | 1 | P51660 m peroxisom | 380 | 1192 | 1 | DNBI HSV2H | P89452 herpes simp |
| 308 | 1 | DHB4 RAT | 735 | 3.1 | 6 | 3.1 | 1 | P97852 r peroxisom | 381 | 1197 | 1 | DNBI HSV2 | P36384 herpes simp |
| 309 | 1 | DHB4 HUMAN | 736 | 3.1 | 6 | 3.1 | 1 | P51659 h peroxisom | 382 | 1233 | 1 | B3A3 RABIT | O18917 oryctolagus |
| 310 | 1 | LGR8 MOUSE | 737 | 3.1 | 6 | 3.1 | 1 | Q91z45 mus musculu | 383 | 1233 | 1 | SAH1 HUMAN | O94885 homo sapien |
| 311 | 1 | ADBI METJA | 748 | 3.1 | 6 | 3.1 | 1 | Q57616 methanococ | 384 | 1247 | 1 | PER2 MOUSE | O54943 mus musculu |
| 312 | 1 | DRS1 YEAST | 752 | 3.1 | 6 | 3.1 | 1 | P32892 saccharomyc | 385 | 1257 | 1 | RBB1 HUMAN | P29374 homo sapien |
| 313 | 1 | LGR8 HUMAN | 754 | 3.1 | 6 | 3.1 | 1 | Q8wxd0 homo sapien | 386 | 1257 | 1 | RPOC MYCPN | P75271 mycoplasma |
| 314 | 1 | SEC6 RAT | 755 | 3.1 | 6 | 3.1 | 1 | Q62825 rattus norv | 387 | 1290 | 1 | PAD3 RAT | Q92340 rattus norv |
| 315 | 1 | SEC6 HUMAN | 756 | 3.1 | 6 | 3.1 | 1 | O60645 homo sapien | 388 | 1337 | 1 | PAD3 HUMAN | Q8tew0 homo sapien |
| 316 | 1 | CHLD TOBAC | 758 | 3.1 | 6 | 3.1 | 1 | O24133 nicotiana t | 389 | 1356 | 1 | TIM DROME | P49021 drosophila |
| 317 | 1 | POT3 ARATH | 775 | 3.1 | 6 | 3.1 | 1 | Q9te38 arabidopsis | 390 | 1421 | 1 | PTPU HUMAN | Q92729 homo sapien |
| 318 | 1 | ARN6 HUMAN | 776 | 3.1 | 6 | 3.1 | 1 | Q15052 homo sapien | 391 | 1430 | 1 | CUT4 SCHPO | Q9urv2 schizosacch |
| 319 | 1 | SN1L RAT | 776 | 3.1 | 6 | 3.1 | 1 | Q9rlu5 rattus norv | 392 | 1458 | 1 | MIS4 SCHPO | Q94813 homo sapien |
| 320 | 1 | FTSK COXBU | 778 | 3.1 | 6 | 3.1 | 1 | P39920 coxiella bu | 393 | 1529 | 1 | S126 SCHPO | Q09725 schizosacch |
| 321 | 1 | SYQ CAEL | 786 | 3.1 | 6 | 3.1 | 1 | O62431 caenorhabdi | 394 | 1583 | 1 | BAIL HUMAN | O14514 homo sapien |
| 322 | 1 | YI01 MYCTU | 786 | 3.1 | 6 | 3.1 | 1 | Q50724 mycobacteri | 395 | 1584 | 1 | TIAM HUMAN | Q13009 homo sapien |
| 323 | 1 | YI01 MYCLE | 792 | 3.1 | 6 | 3.1 | 1 | Q49736 mycobacteri | 396 | 1591 | 1 | RIM1 RAT | Q9jira rattus norv |
| 324 | 1 | CADC HUMAN | 794 | 3.1 | 6 | 3.1 | 1 | P55289 homo sapien | 397 | 1615 | 1 | RIM1 HUMAN | Q86urs5 homo sapien |
| 325 | 1 | UB11 MOUSE | 797 | 3.1 | 6 | 3.1 | 1 | Q99k46 mus musculu | 398 | 1692 | 1 | RIM1 HUMAN | |

| | | | | | | | | | | | |
|-----|---|------|----|-------------|--------|---------------|-----|---|-------------|--------|--------------|
| 399 | 1 | 1744 | 1 | CO4_HUMAN | P01028 | homo sapien | 472 | 1 | Y9K_BPP4 | P12552 | bacterioph |
| 400 | 6 | 1938 | 1 | MYHD_HUMAN | Q9UKX3 | homo sapien | 473 | 1 | Y27A_AERPE | P58322 | aeropyrum p |
| 401 | 6 | 1997 | 1 | OTOF_HUMAN | Q9HC10 | homo sapien | 474 | 1 | RR15_MAIZE | P17703 | zea mays (m |
| 402 | 6 | 2210 | 1 | RRPO_TACV | P20430 | tacaribe vi | 475 | 1 | RR15_ORYZA | P12150 | oryza sativ |
| 403 | 6 | 2492 | 1 | ATRX_HUMAN | P46100 | homo sapien | 476 | 1 | RR15_WHEAT | P20283 | triticum ae |
| 404 | 6 | 2492 | 1 | ATRX_PANTR | Q7YQM4 | pan troglod | 477 | 1 | YORK_TTV1 | P19295 | thermoproc |
| 405 | 6 | 2492 | 1 | ATRX_PONY | Q7YQM3 | pongo pygma | 478 | 1 | DBH_STRDO | Q9XB22 | streptococ |
| 406 | 6 | 2499 | 1 | MRPI_BOVIN | P08169 | bos taurus | 479 | 1 | VI79_FOWPV | Q9J554 | fowlpox vir |
| 407 | 6 | 3060 | 1 | BBEB_HUMAN | Q8WKK8 | homo sapien | 480 | 1 | CH10_STRGN | Q8VT59 | streptococ |
| 408 | 6 | 3214 | 1 | BPAL_HUMAN | Q03001 | homo sapien | 481 | 1 | FTSB_VIBPA | Q871G1 | vibrio para |
| 409 | 6 | 3386 | 1 | POLG_DEN4 | P09866 | d genome po | 482 | 1 | FTSB_VIBSU | Q8DC61 | vibrio vuln |
| 410 | 6 | 4074 | 1 | PKHD_HUMAN | Q8TCZ9 | homo sapien | 483 | 1 | SP3D_BACSU | P15281 | bacillus su |
| 411 | 6 | 4867 | 1 | RYR2_HUMAN | Q92736 | homo sapien | 484 | 1 | CH10_STRBO | Q8XJ15 | streptococ |
| 412 | 6 | 4969 | 1 | RYR2_RABIT | P30957 | oryctolagus | 485 | 1 | DBH_ANASP | P05514 | anaeana sp |
| 413 | 6 | 5035 | 1 | RYR1_PIG | P16960 | sus scrofa | 486 | 1 | DBH_XYLFA | Q87E48 | xylella fas |
| 414 | 6 | 5037 | 1 | RYR1_HUMAN | P11716 | oryctolagus | 487 | 1 | DBH_XYLFT | Q9KUJ3 | vibrio chol |
| 415 | 6 | 5038 | 1 | RYR1_HUMAN | P21817 | homo sapien | 488 | 1 | FTSB_VIECH | P03476 | influenza a |
| 416 | 6 | 5065 | 1 | EPPL_HUMAN | P58107 | homo sapien | 489 | 1 | NRAM_IATKR | O05728 | helicobacte |
| 417 | 6 | 5171 | 1 | BREA_HUMAN | Q94833 | homo sapien | 490 | 1 | VAPD_HELPY | P11830 | saccharopol |
| 418 | 6 | 5348 | 1 | EPPL_MOUSE | Q8X0W0 | mus musculus | 491 | 1 | VLYS_BPAPS | P94797 | francisella |
| 419 | 5 | 26 | 23 | FMK7_PSEAE | Q53391 | pseudomonas | 492 | 1 | ACP_SACER | P58251 | clostridium |
| 420 | 5 | 26 | 24 | PSBR_WHEAT | P12358 | tritium ae | 493 | 1 | CH10_FRATU | P18608 | mus musculu |
| 421 | 5 | 26 | 31 | PETL_PORPU | P48366 | cyanophora | 494 | 1 | CG11_CLOBAB | P00089 | entomospiril |
| 422 | 5 | 26 | 33 | PETM_CVAPA | P48366 | cyanophora | 495 | 1 | CG11_MOUSE | Q24824 | entamoeba h |
| 423 | 5 | 26 | 38 | E2F1_RAT | O09139 | rattus norv | 496 | 1 | PPPB_ENTHI | P03640 | bacterioph |
| 424 | 5 | 26 | 42 | PPPS_RABIT | P55739 | oryctolagus | 497 | 1 | VGE_BPG4 | Q57621 | methanococ |
| 425 | 5 | 26 | 45 | CYC6_PROHO | P81244 | prochloroth | 498 | 1 | Y157_METJA | Q33024 | mycobacteri |
| 426 | 5 | 26 | 50 | ALL6_OLEEU | O24172 | olea europ | 499 | 1 | Y398_MYCLE | P03024 | mycobacteri |
| 427 | 5 | 26 | 51 | LANA_STRPY | P36501 | streptococ | 500 | 1 | CY22_RHOMO | P00088 | rhodospiril |
| 428 | 5 | 26 | 51 | LANB_STRPY | Q54957 | streptococ | 501 | 1 | NUCG_SOYEN | P31174 | glycine max |
| 429 | 5 | 26 | 55 | FIXS_RHIME | P18399 | rhizobium m | 502 | 1 | VMT2_IABAN | P21430 | influenza a |
| 430 | 5 | 26 | 55 | RS21_UREPA | Q9PRL4 | ureaplasma | 503 | 1 | VMT2_IABAN | P36348 | influenza a |
| 431 | 5 | 26 | 58 | SINI_ORILA | P22755 | baacillus li | 504 | 1 | VMT2_IASIN | P10921 | influenza a |
| 432 | 5 | 26 | 59 | RS30_ORILA | Q9W6Y0 | oryzias lat | 505 | 1 | VMT2_IASIN | P03490 | influenza a |
| 433 | 5 | 26 | 60 | RL29_SCHPO | Q92366 | schizosacch | 506 | 1 | VMT2_IASIN | P03490 | influenza a |
| 434 | 5 | 26 | 61 | RS14_LEPIN | Q9XD23 | leptospiro | 507 | 1 | VMT2_IASIN | P03490 | influenza a |
| 435 | 5 | 26 | 61 | YLCB_ECOLI | P77087 | escherichia | 508 | 1 | VMT2_IASIN | P03490 | influenza a |
| 436 | 5 | 26 | 62 | YB53_METJA | Q58553 | methanococ | 509 | 1 | VMT2_IASIN | P03490 | influenza a |
| 437 | 5 | 26 | 62 | YMA5_CABEL | P34521 | caenorhabdi | 510 | 1 | VMT2_IASIN | P03490 | influenza a |
| 438 | 5 | 26 | 63 | COXA_MANSE | O61494 | manduca sex | 511 | 1 | VMT2_IASIN | P03490 | influenza a |
| 439 | 5 | 26 | 65 | SCX4_LEIQH | P83644 | lelurus qui | 512 | 1 | VMT2_IASIN | P03490 | influenza a |
| 440 | 5 | 26 | 67 | CD52_CANFA | Q28896 | canis famli | 513 | 1 | VMT2_IASIN | P03490 | influenza a |
| 441 | 5 | 26 | 67 | CERC_CERCA | Q17313 | ceratitidis c | 514 | 1 | VMT2_IASIN | P03490 | influenza a |
| 442 | 5 | 26 | 68 | MT3_PIG | P55944 | sus scrofa | 515 | 1 | VMT2_IASIN | P03490 | influenza a |
| 443 | 5 | 26 | 70 | YF75_METJA | Q58974 | methanococ | 516 | 1 | VMT2_IASIN | P03490 | influenza a |
| 444 | 5 | 26 | 71 | FTSB_BUCAL | P57496 | buchnera ap | 517 | 1 | VMT2_IASIN | P03490 | influenza a |
| 445 | 5 | 26 | 72 | YCX1_OENBE | P11673 | oenothera b | 518 | 1 | VMT2_IASIN | P03490 | influenza a |
| 446 | 5 | 26 | 76 | VE7_BPVA | P08351 | bovine papi | 519 | 1 | VMT2_IASIN | P03490 | influenza a |
| 447 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 520 | 1 | VMT2_IASIN | P03490 | influenza a |
| 448 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 521 | 1 | VMT2_IASIN | P03490 | influenza a |
| 449 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 522 | 1 | VMT2_IASIN | P03490 | influenza a |
| 450 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 523 | 1 | VMT2_IASIN | P03490 | influenza a |
| 451 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 524 | 1 | VMT2_IASIN | P03490 | influenza a |
| 452 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 525 | 1 | VMT2_IASIN | P03490 | influenza a |
| 453 | 5 | 26 | 77 | APEL_MOUSE | Q9U0Z1 | homo sapien | 526 | 1 | VMT2_IASIN | P03490 | influenza a |
| 454 | 5 | 26 | 79 | IF1C_CHLUV | P56290 | chlorella v | 527 | 1 | VMT2_IASIN | P03490 | influenza a |
| 455 | 5 | 26 | 79 | R17E_SULSO | Q980K7 | sulfolobus | 528 | 1 | VMT2_IASIN | P03490 | influenza a |
| 456 | 5 | 26 | 79 | XJZB_BACSU | Q34891 | bacillus su | 529 | 1 | VMT2_IASIN | P03490 | influenza a |
| 457 | 5 | 26 | 80 | EX7S_BACSU | Q87R68 | vibrio para | 530 | 1 | VMT2_IASIN | P03490 | influenza a |
| 458 | 5 | 26 | 80 | KRHA_SHEEP | Q02958 | ovis aries | 531 | 1 | VMT2_IASIN | P03490 | influenza a |
| 459 | 5 | 26 | 83 | RL27_CHLTR | Q84424 | chlamydia t | 532 | 1 | VMT2_IASIN | P03490 | influenza a |
| 460 | 5 | 26 | 83 | ATPL_VIBPA | P12991 | vibrio para | 533 | 1 | VMT2_IASIN | P03490 | influenza a |
| 461 | 5 | 26 | 84 | ATPL_VIBPA | P12991 | vibrio para | 534 | 1 | VMT2_IASIN | P03490 | influenza a |
| 462 | 5 | 26 | 85 | PDGS_HUMAN | Q8NFU4 | homo sapien | 535 | 1 | VMT2_IASIN | P03490 | influenza a |
| 463 | 5 | 26 | 85 | KR71_SHEEP | Q28580 | ovis aries | 536 | 1 | VMT2_IASIN | P03490 | influenza a |
| 464 | 5 | 26 | 85 | RLX_SULAC | P38613 | sulfolobus | 537 | 1 | VMT2_IASIN | P03490 | influenza a |
| 465 | 5 | 26 | 85 | YSH7_CABEL | P50438 | caenorhabdi | 538 | 1 | VMT2_IASIN | P03490 | influenza a |
| 466 | 5 | 26 | 86 | RBS2_ACECL | P16130 | acetabulari | 539 | 1 | VMT2_IASIN | P03490 | influenza a |
| 467 | 5 | 26 | 86 | VGC_BPPHX | P03635 | bacterioph | 540 | 1 | VMT2_IASIN | P03490 | influenza a |
| 468 | 5 | 26 | 86 | Y926_HAEIN | P44076 | haemophilus | 541 | 1 | VMT2_IASIN | P03490 | influenza a |
| 469 | 5 | 26 | 86 | YB86_CLOBAB | Q87J00 | clostridium | 542 | 1 | VMT2_IASIN | P03490 | influenza a |
| 470 | 5 | 26 | 87 | KR71_HUMAN | Q8LUC3 | homo sapien | 543 | 1 | VMT2_IASIN | P03490 | influenza a |
| 471 | 5 | 26 | 88 | Y4EA_RHSIN | P55424 | rhizobium s | 544 | 1 | VMT2_IASIN | P03490 | influenza a |

| | | | | | | | | | | | | | |
|-----|-----|---|------------|---------|--------------|-----|---|-----|-----|---|-------------|---------|--------------|
| 545 | 107 | 1 | KV6F_MOUSE | P04940 | mus musculus | 618 | 5 | 2.6 | 124 | 1 | RL7_RHOSH | P02397 | rhodobacter |
| 546 | 107 | 1 | KV6G_MOUSE | P04941 | mus musculus | 619 | 5 | 2.6 | 125 | 1 | LR14_SULSO | O93774 | sulfolobus |
| 547 | 107 | 1 | KV6I_MOUSE | P04943 | mus musculus | 620 | 5 | 2.6 | 126 | 1 | ACTR_PAPHA | Q28928 | papio hamad |
| 548 | 107 | 1 | KV6J_MOUSE | P04944 | mus musculus | 621 | 5 | 2.6 | 126 | 1 | PFDA_AVBEA | Q3m4c4 | avena fatua |
| 549 | 107 | 1 | SH3M_HUMAN | Q8bjc5 | homo sapien | 622 | 5 | 2.6 | 126 | 1 | RBS1_ACSECL | P16129 | acetabulari |
| 550 | 107 | 1 | SH3M_MOUSE | Q8bjg73 | mus musculus | 623 | 5 | 2.6 | 126 | 1 | RL7_DESVM | P02393 | desulfovibr |
| 551 | 107 | 1 | YEL2_SCHPO | O13868 | schizosacch | 624 | 5 | 2.6 | 126 | 1 | Y502_RICPR | P29d45 | rickettsia |
| 552 | 108 | 1 | INS_PG | P01315 | sus scrofa | 625 | 5 | 2.6 | 126 | 1 | Y664_CHLMU | Q9Pk09 | chlamydia m |
| 553 | 109 | 1 | PRVA_RANES | P06627 | rana escul | 626 | 5 | 2.6 | 127 | 1 | YP7_AGRU | P03867 | agrobacteri |
| 554 | 109 | 1 | RL3E_METKA | Q8cxj0 | methanopyru | 627 | 5 | 2.6 | 127 | 1 | CRCB_LEPIN | Q8ezs4 | leptospira |
| 555 | 109 | 1 | RLA1_SCHPO | P17476 | schizosacch | 628 | 5 | 2.6 | 127 | 1 | CRCB_PSEAE | Q9hw19 | pseudomonas |
| 556 | 109 | 1 | RLA5_SCHPO | Q9uu78 | schizosacch | 629 | 5 | 2.6 | 127 | 1 | FALP_MOUSE | Q9d159 | mus musculus |
| 557 | 109 | 1 | VE7_HPV39 | P24837 | human papil | 630 | 5 | 2.6 | 127 | 1 | UCK7_KLUUA | P43345 | klyveromyc |
| 558 | 110 | 1 | RPCZ_YEAST | Q04307 | saccharomyc | 631 | 5 | 2.6 | 127 | 1 | Y491_PASMU | Q9cnel | pasteurella |
| 559 | 111 | 1 | KV12_RABIT | P01693 | oryctolagus | 632 | 5 | 2.6 | 127 | 1 | YH9H_ECOLI | P28911 | escherichia |
| 560 | 111 | 1 | PT00_YEAST | P38958 | saccharomyc | 633 | 5 | 2.6 | 127 | 1 | YL35_ARCFU | O28145 | archaeoglob |
| 561 | 111 | 1 | QR15_YEAST | P32344 | saccharomyc | 634 | 5 | 2.6 | 128 | 1 | RL7_STRAT | P29142 | streptomyce |
| 562 | 111 | 1 | RA2A_MAIZE | P46252 | zea mays (m | 635 | 5 | 2.6 | 128 | 1 | Y9S8_MYCTU | Q10819 | mycobacteri |
| 563 | 111 | 1 | RL12_AERPE | Q9V9w9 | aeropyrum p | 636 | 5 | 2.6 | 128 | 1 | YMKD_BACSU | P45871 | bacillus su |
| 564 | 111 | 1 | SDX_THEAC | O84390 | chlamydia t | 637 | 5 | 2.6 | 129 | 1 | FN14_HUMAN | Q9mp84 | homo sapien |
| 565 | 111 | 1 | YHIT_CHLTR | P07188 | drosophila | 638 | 5 | 2.6 | 129 | 1 | LY6E_MOUSE | P03552 | cauliflower |
| 566 | 112 | 1 | CLP4_DROME | P07189 | drosohilla | 640 | 5 | 2.6 | 129 | 1 | VDBP_CAMVD | P03553 | cauliflower |
| 567 | 112 | 1 | VNFG_AZOCH | P15333 | azotobacter | 641 | 5 | 2.6 | 129 | 1 | VDBP_CAMVS | Q02967 | cauliflower |
| 568 | 112 | 1 | Y112_ADE02 | Q89ag5 | buchnera ap | 642 | 5 | 2.6 | 129 | 1 | YABR_ECOLI | P03551 | cauliflower |
| 569 | 112 | 1 | YHIT_BUCBP | P03289 | human adeno | 643 | 5 | 2.6 | 129 | 1 | DHSC_PARDE | P52096 | escherichia |
| 570 | 113 | 1 | RA2B_MAIZE | O24415 | zea mays (m | 644 | 5 | 2.6 | 130 | 1 | INI2_HUMAN | Q59659 | paracoccus |
| 571 | 113 | 1 | YACB_MAIZE | Q11048 | mycobacteri | 645 | 5 | 2.6 | 130 | 1 | INI2_PANTR | P09912 | homo sapien |
| 572 | 114 | 1 | YCV1_MCTU | P56352 | chlorella v | 646 | 5 | 2.6 | 130 | 1 | LY6E_MOUSE | Q28808 | pan troglod |
| 573 | 114 | 1 | TYBP_MOUSE | O54885 | mus musculus | 647 | 5 | 2.6 | 130 | 1 | YQJF_ECOLI | Q64253 | mus musculus |
| 574 | 114 | 1 | VG37_BPM15 | Q05247 | mycobacteri | 648 | 5 | 2.6 | 131 | 1 | C79A_ECOLI | P42619 | escherichia |
| 575 | 114 | 1 | YHIT_BUCAI | P57438 | buchnera ap | 649 | 5 | 2.6 | 131 | 1 | C79B_LOCMI | P45586 | locusta mig |
| 576 | 114 | 1 | XJ74_AQUAE | O67784 | aquifex aeo | 650 | 5 | 2.6 | 131 | 1 | Y293_AQUAE | O66643 | aquifex aeo |
| 577 | 115 | 1 | HYPA_AQUAE | O67133 | styela plic | 651 | 5 | 2.6 | 132 | 1 | ACFS_CULPP | O867x3 | culex pipie |
| 578 | 115 | 1 | PT21_STYPL | P28213 | styela plic | 652 | 5 | 2.6 | 132 | 1 | ACFS_CULQU | O867x2 | culex quing |
| 579 | 115 | 1 | RA2B_ARATH | Q981f7 | arabidopsis | 653 | 5 | 2.6 | 132 | 1 | ACFS_CULQU | O866c9 | culex torre |
| 580 | 115 | 1 | RA2A_ARATH | P51407 | arabidopsis | 654 | 5 | 2.6 | 132 | 1 | C580_CVACA | P48935 | cyanidium c |
| 581 | 115 | 1 | TVC2_MOUSE | P03978 | mus musculus | 655 | 5 | 2.6 | 132 | 1 | CHA2_BOMMO | P08825 | bombyx mori |
| 582 | 115 | 1 | COAD_BPKE | P03674 | bacterioph | 656 | 5 | 2.6 | 132 | 1 | CRG5_XENLA | Q06255 | xenopus lae |
| 583 | 116 | 1 | MSCL_STAEP | Q8cp4 | staphylococ | 657 | 5 | 2.6 | 133 | 1 | CDD_SCHPO | Q09190 | schizosacch |
| 584 | 116 | 1 | RBFA_CLOPE | Q8xjr9 | clostridium | 658 | 5 | 2.6 | 133 | 1 | PYRG_FIBSU | Q939r0 | fibrobacter |
| 585 | 116 | 1 | XKDD_BACSU | P39783 | bacillus su | 659 | 5 | 2.6 | 135 | 1 | PK16_GHATE | P16633 | gracilaria |
| 586 | 116 | 1 | YG10_YEAST | P53222 | saccharomyc | 660 | 5 | 2.6 | 135 | 1 | RS19_PIG | Q29308 | sus scrofa |
| 587 | 116 | 1 | LV0A_HUMAN | P04211 | homo sapien | 661 | 5 | 2.6 | 135 | 1 | TVCA_MOUSE | P06325 | mus musculus |
| 588 | 117 | 1 | SP41_HUMAN | Q16550 | homo sapien | 662 | 5 | 2.6 | 136 | 1 | CTD9_MOUSE | Q9d975 | mus musculus |
| 589 | 117 | 1 | SP42_MOUSE | Q9z199 | mus musculus | 663 | 5 | 2.6 | 136 | 1 | RS9_MYCPU | Q98q72 | mycoplasma |
| 590 | 117 | 1 | Y051_RICCN | Q92j16 | rickettsia | 664 | 5 | 2.6 | 137 | 1 | YCR5_YEAST | P25352 | saccharomyc |
| 591 | 117 | 1 | Y13K_HCMVA | P03236 | human cytom | 665 | 5 | 2.6 | 137 | 1 | CTD9_HUMAN | Q9bvt0 | homo sapien |
| 592 | 118 | 1 | Y687_THEMA | Q9wz13 | thermotoga | 666 | 5 | 2.6 | 137 | 1 | IF2B_ARCFU | P27958 | archaeoglob |
| 593 | 118 | 1 | Y13K_HCMVA | P59942 | homo sapien | 667 | 5 | 2.6 | 137 | 1 | MO4H_LIBEM | P56688 | libinia ema |
| 594 | 119 | 1 | MCD1_HUMAN | P00614 | oxyuranus s | 668 | 5 | 2.6 | 138 | 1 | RL32_SULSO | Q9ux90 | sulfolobus |
| 595 | 119 | 1 | RL24_METVA | P14034 | methanococ | 669 | 5 | 2.6 | 138 | 1 | YUXK_BACSU | P25097 | simulium ir |
| 596 | 119 | 1 | RS13_NITEU | P59755 | nitrosomona | 670 | 5 | 2.6 | 138 | 1 | YMSP_IRV22 | P51307 | porphyra pu |
| 597 | 119 | 1 | SSB1_ANASP | Q8z0k3 | anabaena sp | 671 | 5 | 2.6 | 139 | 1 | FK16_PORPU | O83766 | treponema p |
| 598 | 119 | 1 | DAN3_YEAST | P38155 | saccharomyc | 672 | 5 | 2.6 | 139 | 1 | Y787_TBPEA | P83179 | brevicorype |
| 599 | 120 | 1 | GALP_PIG | Q9tt95 | sus scrofa | 673 | 5 | 2.6 | 140 | 1 | MYRO_BREBR | Q09389 | caenorhabdi |
| 600 | 120 | 1 | NU3C_ANTFO | Q31792 | anthoceros | 674 | 5 | 2.6 | 140 | 1 | YR43_CABEL | P56384 | mus musculus |
| 601 | 120 | 1 | PAUL_YEAST | P38924 | saccharomyc | 675 | 5 | 2.6 | 141 | 1 | AT93_MOUSE | O30976 | bruceella ab |
| 602 | 120 | 1 | PAU2_YEAST | P32612 | saccharomyc | 676 | 5 | 2.6 | 141 | 1 | FUR_BRUAB | O8ifz8 | bruceella me |
| 603 | 120 | 1 | PAU6_YEAST | P52921 | saccharomyc | 677 | 5 | 2.6 | 141 | 1 | FUR_BRUSE | O8ifz5 | bruceella su |
| 604 | 120 | 1 | YG65_YEAST | P53343 | saccharomyc | 678 | 5 | 2.6 | 141 | 1 | CDD_YEAST | Q06549 | saccharomyc |
| 605 | 120 | 1 | YGZF_YEAST | P35055 | saccharomyc | 679 | 5 | 2.6 | 142 | 1 | CSTB_MOUSE | P32766 | mus musculus |
| 606 | 120 | 1 | YHE6_YEAST | P38725 | saccharomyc | 680 | 5 | 2.6 | 142 | 1 | RBFA_PROMM | Q7v418 | prochloroco |
| 607 | 120 | 1 | CRNF_LYNST | P91758 | lymnaea sta | 681 | 5 | 2.6 | 142 | 1 | YOX1_CABEL | Q09557 | caenorhabdi |
| 608 | 121 | 1 | RS6_RICCN | Q22jk3 | rickettsia | 682 | 5 | 2.6 | 142 | 1 | HMGB_TETH | P40626 | tetrahymena |
| 609 | 121 | 1 | ACFM_ARATH | P5665 | arabidopsis | 683 | 5 | 2.6 | 143 | 1 | Y771_METH | O26865 | methanobact |
| 610 | 122 | 1 | CH10_AQUAE | O67942 | aquifex aeo | 684 | 5 | 2.6 | 143 | 1 | CS60_RECUM | P80481 | reclinomona |
| 611 | 122 | 1 | CH5_PENMO | Q97387 | penaeus mon | 685 | 5 | 2.6 | 144 | 1 | RS19_HUMAN | P39019 | homo sapien |
| 612 | 122 | 1 | SELH_HUMAN | Q8lqg5 | homo sapien | 686 | 5 | 2.6 | 144 | 1 | YB8A_YEAST | P17074 | rattus norv |
| 613 | 122 | 1 | YBEC_ECOLI | P33668 | escherichia | 687 | 5 | 2.6 | 144 | 1 | SODM_STEPO | P238354 | saccharomyc |
| 614 | 122 | 1 | YFC5_SHEPR | Q02482 | shewanella | 688 | 5 | 2.6 | 144 | 1 | | O54266 | streptococc |
| 615 | 122 | 1 | LSM6_YEAST | P06406 | saccharomyc | 689 | 5 | 2.6 | 145 | 1 | | | |
| 616 | 123 | 1 | RR13_CYAME | P59758 | cyanidiosch | 690 | 5 | 2.6 | 145 | 1 | | | |
| 617 | 123 | 1 | | | | | 5 | 2.6 | | | | | |

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|-----|---|------------|---------|--------------|-----|---|-----|---|------------|--------|--------------|
| 691 | 1 | SSIK_STRPT | Q33702 | streptomyce | 764 | 1 | 158 | 1 | NUGC_SPIOB | Q9m3ml | spinacia ol |
| 692 | 1 | YTKA_BACSU | P40768 | bacillus su | 765 | 1 | 158 | 1 | NUGC_TOBAC | P12201 | nicotiana t |
| 693 | 1 | HBB1_MOUSE | P02088 | mus musculus | 766 | 1 | 159 | 1 | ATPF_CLOAB | O05098 | clostridium |
| 694 | 1 | HBB1_RAT | P02091 | rattus norv | 767 | 1 | 159 | 1 | IF5A_DROME | O9gu68 | clostridila |
| 695 | 1 | HBB2_MOUSE | P02089 | mus musculus | 768 | 1 | 159 | 1 | NUGC_MAIZE | P19124 | oryza may (m |
| 696 | 1 | HBB_MELME | P02055 | meles meles | 769 | 1 | 159 | 1 | NUGC_ORISA | P12200 | zea sativ |
| 697 | 1 | YIAC_ECOLI | P37664 | escherichia | 770 | 1 | 159 | 1 | NUGC_WHEAT | Q95h60 | tritium ae |
| 698 | 1 | CRCB_STAMM | Q99t86 | staphylococ | 771 | 1 | 159 | 1 | RL22_THEMA | P37851 | thermotoga |
| 699 | 1 | CRCB_STAMM | Q9m04 | staphylococ | 772 | 1 | 159 | 1 | SMG_VIBPA | Q87k48 | vibrio para |
| 700 | 1 | CRCB_STAMM | Q88w99 | lactobacilli | 773 | 1 | 159 | 1 | VGLL_VZVD | P09308 | varicella-z |
| 701 | 1 | IL4_MESAU | Q60440 | mesocricetu | 774 | 1 | 159 | 1 | Y165_CLOTE | Q899k8 | clostridium |
| 702 | 1 | MSRB_CLOPE | Q8XJ26 | clostridium | 775 | 1 | 159 | 1 | YQ00_CLOPE | O8xh85 | clostridium |
| 703 | 1 | RS12_METVA | P14040 | methanococc | 776 | 1 | 160 | 1 | CCMH_BRAJA | P45405 | bradyrhizob |
| 704 | 1 | RL16_CAEBL | Q10129 | caenorhabdi | 777 | 1 | 160 | 1 | HS21_HELAN | P46516 | helianthus |
| 705 | 1 | UCRH_YEAST | P00127 | saccharomyc | 778 | 1 | 160 | 1 | NU6M_PARLI | P12777 | paracentrot |
| 706 | 1 | FKXB_ECOLI | P22563 | escherichia | 779 | 1 | 160 | 1 | UI95_HUMAN | Q9h5x1 | homo sapien |
| 707 | 1 | MYG_GALGA | P14397 | galeorhinus | 780 | 1 | 160 | 1 | UI95_MOUSE | Q8dc12 | mus musculus |
| 708 | 1 | MYG_HETPO | P02206 | heterodontu | 781 | 1 | 160 | 1 | YVYG_BACSU | P39808 | bacillus su |
| 709 | 1 | ARGR_BACLI | O86130 | bacillus li | 782 | 1 | 160 | 1 | HBPL_PARAD | P04396 | parapsonia |
| 710 | 1 | PER1_PEA | P09911 | pisum sativ | 783 | 1 | 161 | 1 | ID4_MOUSE | P47928 | homo sapien |
| 711 | 1 | FLBY_CAUCR | P33977 | caulobacter | 784 | 1 | 161 | 1 | ID4_MOUSE | P41139 | mus musculus |
| 712 | 1 | PPDD_HAEIN | P44623 | haemophilus | 785 | 1 | 161 | 1 | RRAI_VIBCH | Q9kpk1 | vibrio chol |
| 713 | 1 | Y919_METVA | Q58329 | methanococc | 786 | 1 | 161 | 1 | VANZ_ENTFC | Q06242 | enterococcu |
| 714 | 1 | YK05_AQUAE | O67808 | aquifex aeo | 787 | 1 | 162 | 1 | CRIZ_ALGSP | O44262 | alcaligenes |
| 715 | 1 | ALL5_HEVER | Q39967 | hevea bras | 788 | 1 | 162 | 1 | EL18_ADST1 | P06439 | tupaia aden |
| 716 | 1 | GRDA_CLOPU | P26970 | clostridium | 789 | 1 | 162 | 1 | GTR4_CANFA | Q9xst2 | canis famli |
| 717 | 1 | NRDI_MYCTU | P95107 | mycobacteri | 790 | 1 | 162 | 1 | YAB4_STRCP | P00308 | synechococc |
| 718 | 1 | RL15_RICPR | Q9xc84 | ricketsia | 791 | 1 | 163 | 1 | ELBS_ADEL2 | Q9f2u7 | streptomyce |
| 719 | 1 | RS13_HUMAN | Q02546 | homo sapien | 792 | 1 | 163 | 1 | YAB4_STRCP | P04492 | human adeno |
| 720 | 1 | RS13_ICTPU | P47772 | ictalurus p | 793 | 1 | 163 | 1 | PP01_PHYPO | Q13526 | homo sapien |
| 721 | 1 | RS13_XENLA | P49393 | xenopus lae | 794 | 1 | 163 | 1 | SAK_STEAM | Q94702 | physarum po |
| 722 | 1 | RS13_YEAST | P05756 | saccharomyc | 795 | 1 | 163 | 1 | SAK_STEAM | P15240 | bacterioph |
| 723 | 1 | SSB_THETN | O8-6m2 | thermoanaer | 796 | 1 | 163 | 1 | YF62_STR43 | P00802 | staphylococ |
| 724 | 1 | SSRP_BACTN | Q8abd1 | bacteroides | 797 | 1 | 163 | 1 | YF62_STR43 | Q95230 | papio hamad |
| 725 | 1 | YF59_MYCLE | Q925j2 | mycobacteri | 798 | 1 | 163 | 1 | Y057_NPVOP | O10315 | argyria pseu |
| 726 | 1 | CRPE_CHLTR | P26757 | chlamydia t | 799 | 1 | 163 | 1 | YITK_BACSU | O06746 | bacillus su |
| 727 | 1 | SP17_HUMAN | Q15506 | homo sapien | 800 | 1 | 164 | 1 | ID1_RAT | P41135 | rattus norv |
| 728 | 1 | SP17_NACFA | Q19021 | macaca fasc | 801 | 1 | 164 | 1 | MAFF_HUMAN | Q9ulx9 | homo sapien |
| 729 | 1 | TERS_BPSF6 | Q38627 | bacterioph | 802 | 1 | 164 | 1 | MCRD_METVA | Q58253 | methanococc |
| 730 | 1 | UBCK_DROME | Q45584 | bacillus su | 803 | 1 | 164 | 1 | GA45_RAT | P48317 | rattus norv |
| 731 | 1 | YBCK_BACSU | P42108 | bacillus su | 804 | 1 | 165 | 1 | NRG7_HUMAN | Q16617 | homo sapien |
| 732 | 1 | YXAI_BACSU | P12942 | pisum sativ | 805 | 1 | 165 | 1 | RS13_SULSO | P59586 | sulfolobus |
| 733 | 1 | HS21_PRA | Q99t10 | staphylococ | 806 | 1 | 165 | 1 | Y473_STRPY | Q9a143 | streptococc |
| 734 | 1 | PHEB_STAMM | O8ztv0 | pyrobaculum | 807 | 1 | 165 | 1 | YF62_STR43 | Q8e441 | streptococc |
| 735 | 1 | RS13_PYRAE | Q58753 | methanococc | 808 | 1 | 166 | 1 | NUOE_ECOLI | P33601 | escherichia |
| 736 | 1 | ID58_METJA | Q58958 | methanococc | 809 | 1 | 166 | 1 | NUOE_SALTY | P33903 | salmonella |
| 737 | 1 | YFJ6_BACSU | O67706 | aquifex aeo | 810 | 1 | 166 | 1 | RR43_ARATH | Q9fh13 | arabidopsis |
| 738 | 1 | YFJ6_BACSU | P02613 | patinopecte | 811 | 1 | 167 | 1 | CHCC_ANTPO | P08930 | anthraea p |
| 739 | 1 | YI54_AQUAE | O67706 | aquifex aeo | 812 | 1 | 167 | 1 | YB20_AQUAE | O67200 | aquifex aeo |
| 740 | 1 | MLR_FATSP | Q9x0r7 | thermotoga | 813 | 1 | 167 | 1 | YF57_ARCFU | O28715 | archaeoglob |
| 741 | 1 | SODC_YEAST | P00445 | saccharomyc | 814 | 1 | 168 | 1 | ID1_MOUSE | P20067 | mus musculus |
| 742 | 1 | PFDA_AERPE | Q9y428 | aeropyrum p | 815 | 1 | 168 | 1 | ILVH_METH | O27492 | methanobact |
| 743 | 1 | PFDA_HALN1 | P38457 | capparis ma | 816 | 1 | 168 | 1 | RIAB_CVCAI | O27492 | methanobact |
| 744 | 1 | YMI3_MARPO | P30233 | marchantia | 817 | 1 | 169 | 1 | AROK_COREF | P36697 | canine ente |
| 745 | 1 | 2SS2_CAFPA | P04037 | saccharomyc | 818 | 1 | 169 | 1 | AROK_COREF | Q8fc30 | corynebacte |
| 746 | 1 | COX4_YEAST | P41134 | homo sapien | 819 | 1 | 169 | 1 | CS60_BOVIN | Q9x5d1 | corynebacte |
| 747 | 1 | ID1_HUMAN | Q29175 | sus scrofa | 820 | 1 | 169 | 1 | YF62_STR43 | P35720 | bos taurus |
| 748 | 1 | KE4_PIG | Q9x0r7 | thermotoga | 821 | 1 | 169 | 1 | YF62_STR43 | P02531 | rana tempor |
| 749 | 1 | MGSA_THEMA | Q9ppw6 | ureaplasma | 822 | 1 | 170 | 1 | MOAC_BACSU | P21678 | bacterioph |
| 750 | 1 | RS7_UREPA | O55827 | synechocyst | 823 | 1 | 170 | 1 | NU2M_ANOAL | P21678 | bacterioph |
| 751 | 1 | Y481_SYNY3 | P13543 | aequiptecten | 824 | 1 | 170 | 1 | YF64_METJA | Q44849 | borrelia bu |
| 752 | 1 | MLR_AEQIR | Q8t-xv5 | methanopyru | 825 | 1 | 171 | 1 | CYP7_CAEEL | O05520 | bacillus su |
| 753 | 1 | MOAC_METKA | Q8t-vb1 | methanopyru | 826 | 1 | 171 | 1 | H1_ECHCR | O05520 | bacillus su |
| 754 | 1 | PYRI_METKA | Q9aig8 | carsonella | 827 | 1 | 171 | 1 | LSPA_PSEPK | Q33636 | anopheles a |
| 755 | 1 | RS7_CARRU | P08367 | escherichia | 828 | 1 | 171 | 1 | RIMM_BACAA | Q58959 | methanococc |
| 756 | 1 | CREA_ECOLI | Q8kc25 | chlorobium | 829 | 1 | 171 | 1 | YF64_METJA | P52015 | caenorhabdi |
| 757 | 1 | ISPF_CHLTE | Q8kc25 | chlorobium | 830 | 1 | 171 | 1 | CYP7_CAEEL | P02257 | echinolampa |
| 758 | 1 | Y406_MYCPN | Q50325 | mycoplasma | 831 | 1 | 172 | 1 | HS21_HELAN | Q88q91 | pseudomonas |
| 759 | 1 | CT35_MOUSE | Q3crd4 | mus musculus | 832 | 1 | 172 | 1 | CRBS_CHICO | Q81w15 | bacillus an |
| 760 | 1 | NUGC_ARATH | P56754 | arabidopsis | 833 | 1 | 172 | 1 | NU6M_MOUSE | Q57374 | haemophilus |
| 761 | 1 | NUGC_LOTJA | Q9bbt6 | lotus japon | 834 | 1 | 172 | 1 | RS13_SULTO | P48647 | chiloscylli |
| 762 | 1 | NUGC_LUPLU | P92309 | lutinus lut | 835 | 1 | 172 | 1 | SSRD_MOUSE | P03925 | mus musculus |
| 763 | 1 | NUGC_OENHO | Q9mtp3 | oenothera h | 836 | 1 | 172 | 1 | YNCA_ECOLI | Q62186 | mus musculus |

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|-----|---|------------|--------|-------------|-----|---|-----|-----|---|------------|--------|--------------|
| 837 | 1 | FR13_RANCA | P07797 | iana catesb | 910 | 5 | 2.6 | 185 | 1 | Y754_METUA | Q58164 | methanococc |
| 838 | 1 | MURS_FELCA | P41691 | felis silve | 911 | 5 | 2.6 | 185 | 1 | YCF4_BRAOL | Q31910 | brassica ol |
| 839 | 1 | MURS_HUMAN | Q02045 | homo sapien | 912 | 5 | 2.6 | 186 | 1 | AROK_BACSU | P37944 | bacillus su |
| 840 | 1 | PECF_ANASP | P35798 | anabaena sp | 913 | 5 | 2.6 | 186 | 1 | DMML_METFL | Q50425 | methyllobaci |
| 841 | 1 | RBS2_ACENE | P16135 | acetabulari | 914 | 5 | 2.6 | 186 | 1 | Y783_METJA | Q58193 | methanococc |
| 842 | 1 | SSRD_HUMAN | P51571 | homo sapien | 915 | 5 | 2.6 | 186 | 1 | YCF4_OENHO | Q9mt11 | oenothera h |
| 843 | 1 | SSRD_RAT | Q07984 | rattus norv | 916 | 5 | 2.6 | 187 | 1 | Y503_TREPA | Q83516 | treponema p |
| 844 | 1 | YU74_METWA | Q89k5 | methanosarc | 917 | 5 | 2.6 | 187 | 1 | YCF4_MESVI | Q9mun8 | mesostigma |
| 845 | 1 | PAF3_MOUSE | Q89049 | mus musculu | 918 | 5 | 2.6 | 188 | 1 | GTS2_CAEEL | O16115 | caenorhabdi |
| 846 | 1 | PAF3_RAT | P42854 | rattus norv | 919 | 5 | 2.6 | 188 | 1 | HSLV_CAUCR | Q7a239 | caulobacter |
| 847 | 1 | YP08_METAC | Q8cm96 | methanosarc | 920 | 5 | 2.6 | 188 | 1 | YCF4_GLOVI | Q7uph6 | gloeobacter |
| 848 | 1 | CRG3_XENLA | P55940 | xenopus lae | 921 | 5 | 2.6 | 189 | 1 | KTHI_SULSO | Q93341 | caenorhabdi |
| 849 | 1 | CSF3_CANFA | P35834 | canis famli | 922 | 5 | 2.6 | 189 | 1 | LVN1_LYTVA | P15262 | lytechinus |
| 850 | 1 | MEF3_BOVIN | Q28103 | bos taurus | 923 | 5 | 2.6 | 189 | 1 | P8BY_ARATH | Q49347 | arabidopsis |
| 851 | 1 | PAP1_MOUSE | P35230 | mus musculu | 924 | 5 | 2.6 | 189 | 1 | RS9_CAEEL | Q20228 | caenorhabdi |
| 852 | 1 | RBS_BATOE | P26985 | batophora o | 925 | 5 | 2.6 | 189 | 1 | 3MGH_DEIRA | Q9rsq0 | deinococcus |
| 853 | 1 | AROK_CHLPN | Q926m1 | chlamydia p | 926 | 5 | 2.6 | 190 | 1 | APOM_RAT | P14630 | rattus norv |
| 854 | 1 | ATPF_SYNPI | Q05365 | synchococc | 927 | 5 | 2.6 | 190 | 1 | HDED_ECOLI | P26603 | escherichia |
| 855 | 1 | HPRT_VIBHA | P18134 | vibrio harv | 928 | 5 | 2.6 | 190 | 1 | RT23_HUMAN | Q9yjd9 | homo sapien |
| 856 | 1 | IDI_EHOCA | Q8cmk6 | staphylococ | 929 | 5 | 2.6 | 190 | 1 | VIS1_HUMAN | P28677 | homo sapien |
| 857 | 1 | MOAB_STAEP | Q95695 | arabidopsis | 931 | 5 | 2.6 | 190 | 1 | VIS2_RAT | P35332 | rattus norv |
| 858 | 1 | NU6C_ARATH | P18509 | n pituitary | 932 | 5 | 2.6 | 191 | 1 | PGHD_SHEEP | Q9xsm0 | ovis aries |
| 859 | 1 | PACA_HUMAN | Q8ftn0 | corynebacte | 933 | 5 | 2.6 | 191 | 1 | YL27_STRCO | P40182 | streptomyce |
| 860 | 1 | ARGR_COREF | Q8k9u8 | buchnera ap | 934 | 5 | 2.6 | 192 | 1 | MOBA_NEIMA | Q9juu5 | neisseria m |
| 861 | 1 | HPRT_BUCAP | Q9rtv5 | deinococcus | 935 | 5 | 2.6 | 192 | 1 | Y857_METTH | O26945 | methanobact |
| 862 | 1 | LED1_DRIRA | Q8va22 | mus musculu | 936 | 5 | 2.6 | 192 | 1 | YC08_YEAST | P37261 | saccharomyc |
| 863 | 1 | RT23_MOUSE | P57291 | buchnera ap | 937 | 5 | 2.6 | 193 | 1 | CERR_MOUSE | P23435 | homo sapien |
| 864 | 1 | HPRT_BUCAL | P36766 | escherichia | 938 | 5 | 2.6 | 193 | 1 | CERR_MOUSE | Q9x171 | mus musculu |
| 865 | 1 | HPRT_ECOLI | Q33799 | salmonella | 939 | 5 | 2.6 | 194 | 1 | CLPI_CYPAP | Q36863 | cyanophora |
| 866 | 1 | HPRT_SALTY | Q927t3 | listeria in | 940 | 5 | 2.6 | 194 | 1 | FLR_DESGI | Q9kat1 | desulfovibr |
| 867 | 1 | RPOE_LISMO | Q8y494 | listeria mo | 941 | 5 | 2.6 | 194 | 1 | KADI_MOUSE | Q9roy5 | mus musculu |
| 868 | 1 | QOHR_BACSU | P54516 | bacillus su | 942 | 5 | 2.6 | 194 | 1 | KADI_MOUSE | P39069 | rattus norv |
| 869 | 1 | ATPD_BACSU | Q8cmj4 | staphylococ | 943 | 5 | 2.6 | 194 | 1 | KADI_MOUSE | P29999 | african swi |
| 870 | 1 | ATPF_SYNPI | P27181 | synchocyst | 944 | 5 | 2.6 | 194 | 1 | VP30_ASFE7 | Q58069 | methanococc |
| 871 | 1 | HPRT_HAIN | P45078 | haemophilus | 945 | 5 | 2.6 | 194 | 1 | Y653_METJA | Q9rrf9 | deinococcus |
| 872 | 1 | Y279_THEVO | Q97c26 | thermoplasm | 946 | 5 | 2.6 | 194 | 1 | YD16_HABIN | Q8p319 | xanthomonas |
| 873 | 1 | ATPD_ENTHR | P26680 | enterococcu | 947 | 5 | 2.6 | 195 | 1 | PAAD_DEIRA | P18555 | african swi |
| 874 | 1 | RL10_TREPA | Q83267 | treponema p | 948 | 5 | 2.6 | 195 | 1 | TATB_XANCP | P40958 | saccharomyc |
| 875 | 1 | RL5_HELPF | Q9zj84 | helicobacte | 949 | 5 | 2.6 | 196 | 1 | KITH_ASFB7 | Q8v7b1 | arabidopsis |
| 876 | 1 | RL5_HELPF | P56033 | helicobacte | 950 | 5 | 2.6 | 196 | 1 | MAD2_YEAST | Q8v7b1 | arabidopsis |
| 877 | 1 | TRIF_HUMAN | P13412 | mus musculu | 951 | 5 | 2.6 | 196 | 1 | SOHI_ARATH | P10944 | escherichia |
| 878 | 1 | TRIF_MOUSE | P27643 | oryctolagus | 952 | 5 | 2.6 | 196 | 1 | UHPA_ECOLI | P34204 | african swi |
| 879 | 1 | TRIF_RABIT | P27643 | oryctolagus | 953 | 5 | 2.6 | 196 | 1 | VP32_ASFB7 | Q8p7u5 | xanthomonas |
| 880 | 1 | TRIF_RAT | Q9h1p8 | thermoplasm | 954 | 5 | 2.6 | 196 | 1 | YP13_XANCP | Q8p7u5 | xanthomonas |
| 881 | 1 | Y179_THRAC | Q34565 | caenorhabdi | 955 | 5 | 2.6 | 196 | 1 | YQ89_XANCP | Q8p7u5 | xanthomonas |
| 882 | 1 | YNV2_CAEEL | Q40298 | macrocystis | 956 | 5 | 2.6 | 197 | 1 | CFI2_MEDSA | P28013 | medicago sa |
| 883 | 1 | FCPD_MACEY | P37171 | thodobacter | 957 | 5 | 2.6 | 197 | 1 | DEM1_PHYSA | P05422 | phyllomedus |
| 884 | 1 | HPRT_RHOCA | P04261 | bos taurus | 958 | 5 | 2.6 | 197 | 1 | RECR_FUSNN | Q8rg96 | fusobacteri |
| 885 | 1 | K2C3_BOVIN | P04260 | bos taurus | 959 | 5 | 2.6 | 197 | 1 | RL18_SULAC | O05640 | sulfolobus |
| 886 | 1 | K2C3_BOVIN | P04260 | bos taurus | 960 | 5 | 2.6 | 197 | 1 | YCB7_SEDE | P29940 | pseudomonas |
| 887 | 1 | PUR5_STRFP | P40178 | streptomyce | 961 | 5 | 2.6 | 197 | 1 | YCB7_SEDE | P05421 | phyllomedus |
| 888 | 1 | RBS1_ACENE | P16134 | acetabulari | 962 | 5 | 2.6 | 198 | 1 | DEM2_PHYSA | Q61907 | mus musculu |
| 889 | 1 | RBS3_ACENE | P16136 | acetabulari | 963 | 5 | 2.6 | 198 | 1 | PEMT_MOUSE | Q8388 | rattus norv |
| 890 | 1 | RBS4_ACCEL | P16132 | acetabulari | 964 | 5 | 2.6 | 198 | 1 | PEMT_MOUSE | Q00579 | streptococc |
| 891 | 1 | RBS4_ACCEL | P16137 | acetabulari | 965 | 5 | 2.6 | 198 | 1 | RECU_STRPN | P38034 | streptococc |
| 892 | 1 | RBS6_ACCEL | Q38692 | acetabulari | 966 | 5 | 2.6 | 198 | 1 | TSAA_HELPJ | P56876 | helicobacte |
| 893 | 1 | RL5X_THETH | P41201 | thermus the | 967 | 5 | 2.6 | 198 | 1 | YHCS_BACSU | P54603 | bacillus su |
| 894 | 1 | RL5X_THETH | P42315 | thermus the | 968 | 5 | 2.6 | 199 | 1 | AROK_MYCLE | Q8ccs5 | mycobacteri |
| 895 | 1 | RL5_THETH | P42315 | thermus the | 969 | 5 | 2.6 | 199 | 1 | AROK_MYCLE | Q8ccs5 | mycobacteri |
| 896 | 1 | AROK_BACHD | Q9kfh9 | bacillus ha | 970 | 5 | 2.6 | 200 | 1 | ISPP_BRAJA | P30961 | bradyrhizob |
| 897 | 1 | AROK_OCEIH | Q9kfh9 | bacillus ha | 971 | 5 | 2.6 | 200 | 1 | ISPP_BRAJA | P30961 | bradyrhizob |
| 898 | 1 | HMAL_HUMAN | Q9uj13 | homo sapien | 972 | 5 | 2.6 | 200 | 1 | NADD_SYNY3 | P73246 | synchocyst |
| 899 | 1 | RBS3_ACCEL | P16131 | acetabulari | 973 | 5 | 2.6 | 200 | 1 | PCXA_PSEPU | P00436 | pseudomonas |
| 900 | 1 | RBS5_ACENE | P16138 | acetabulari | 974 | 5 | 2.6 | 200 | 1 | RUVA_STAEP | Q8cs90 | staphylococ |
| 901 | 1 | TERS_EPSPF | P54307 | bacterioph | 975 | 5 | 2.6 | 201 | 1 | YDJM_ECOLI | P76209 | escherichia |
| 902 | 1 | ATPD_SYNPI | Q05374 | synchococc | 976 | 5 | 2.6 | 201 | 1 | ADEN_ADEB2 | Q40958 | equine aden |
| 903 | 1 | K501_ACTCH | P43393 | actinidia c | 977 | 5 | 2.6 | 201 | 1 | RT10_HUMAN | Q8ntu7 | homo sapien |
| 904 | 1 | RBS5_ACCEL | P16133 | acetabulari | 978 | 5 | 2.6 | 201 | 1 | CERL_HUMAN | P82664 | homo sapien |
| 905 | 1 | RS13_SULAC | P19470 | sulfolobus | 979 | 5 | 2.6 | 202 | 1 | CTD6_HUMAN | Q9p720 | neurospora |
| 906 | 1 | YQFB_PSEAE | Q9htw5 | pseudomonas | 980 | 5 | 2.6 | 202 | 1 | RL16_NEUCR | P48230 | homo sapien |
| 907 | 1 | FLAV_AQUAE | Q67866 | aquifex aeo | 981 | 5 | 2.6 | 202 | 1 | T484_HUMAN | Q06241 | enterococcu |
| 908 | 1 | IF3_COXBU | Q83c11 | coxiella bu | 982 | 5 | 2.6 | 202 | 1 | VANX_ENTFC | | |
| 909 | 1 | RFBC_ECOLI | P37745 | escherichia | | | | | | | | |

| FT | METAL | 89 | 89 | CALCIUM (VIA CARBONYL OXYGEN) |
|-----------------------|--|-------------------------|---|---|
| FT | METAL | 91 | 91 | (BY SIMILARITY). |
| FT | METAL | 93 | 93 | CALCIUM (VIA CARBONYL OXYGEN) |
| FT | METAL | 116 | 116 | (BY SIMILARITY). |
| FT | CONFLICT | 157 | 157 | CALCIUM (BY SIMILARITY). |
| FT | SEQUENCE | 195 AA; | 21659 MW; | MISSING (IN REF. 1). |
| FT | SEQUENCE | 195 AA; | 21659 MW; | C00C817F81D68A70 CRC64; |
| Query Match | | 70.6%; | Score 137; | DB 1; Length 195; |
| Best Local Similarity | | 100.0%; | Pred. No. 6.1e-134; | |
| Matches 137; | Conservative | 0; | Mismatches 0; | Indels 0; Gaps 0; |
| QY | 1 | MKLASGFLVLTSLGGLAQSDTSP | TEESYSDWGRLHURGSFESVNSYFDSFLELLGGK | 60 |
| Db | 1 | MKLASGFLVLTSLGGLAQSDTSP | TEESYSDWGRLHURGSFESVNSYFDSFLELLGGK | 60 |
| QY | 61 | NGVCQYRCYRGKAPMPRGYK | POEPNGCGSYFGLKVPESMDLIGIPAMTKCCNOLDVCYD | 120 |
| Db | 61 | NGVCQYRCYRGKAPMPRGYK | POEPNGCGSYFGLKVPESMDLIGIPAMTKCCNOLDVCYD | 120 |
| QY | 121 | TCGANKYRCDKAFRWCL | 137 | |
| Db | 121 | TCGANKYRCDKAFRWCL | 137 | |
| RESULT 2 | | | | |
| PA2Z MOUSE | | | | |
| ID | PA2Z MOUSE | STANDARD; | PRT; | 195 AA. |
| AC | Q99P27; | | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Group XIII secretory phospholipase A2-like protein precursor (GXIII sPLA2-like). | | | |
| GN | PLA2G13 OR FKSG71. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | | | |
| OX | NCBI_Taxid=10090; | | | |
| RP | [1] | | | |
| RC | SEQUENCE FROM N.A. | | | |
| RA | STRAIN=C57BL/6 x DBA; | | | |
| RA | Wang Y.-G., Gong L.; | | | |
| RT | "Cloning and characterization of FKSG71, a novel gene encoding group | | | |
| RT | XIII secreted phospholipase A2."; | | | |
| RL | Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -!- FUNCTION: Not known; does not seem to have catalytic activity. | | | |
| CC | -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity). | | | |
| CC | -!- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -!- SIMILARITY: Belongs to the phospholipase A2 family. | | | |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announcement | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| DR | EMBL; AF339738; AAK01739.1; -- | | | |
| DR | MGD; MGI:1917086; Pla2g13. | | | |
| DR | InterPro; IPR000886; ER_target_S. | | | |
| DR | InterPro; IPR001211; PhospholipaseA2. | | | |
| DR | PROSITE; PS00119; PA2 ASP; FALSE_NEG. | | | |
| DR | PROSITE; PS00118; PA2 HIS; FALSE_NEG. | | | |
| DR | PROSITE; PS00014; ER_TARGET; UNKNOWN_1. | | | |
| KW | Calcium; Signal. | | | |
| FT | SIGNAL | 1 | 19 | POTENTIAL. |
| FT | CHAIN | 20 | 195 | GROUP XIII SECRETORY PHOSPHOLIPASE A2- LIKE PROTEIN. |
| FT | METAL | 89 | 89 | CALCIUM (VIA CARBONYL OXYGEN) |

Mon May 17 11:51:02 2004

T METAL 91 91 (BY SIMILARITY)
T T METAL 91 91 (BY SIMILARITY)
T T METAL 93 93 (BY SIMILARITY)
T T METAL 116 116 (BY SIMILARITY)
T T METAL 195 AA; 21736 MW; 86F8E653BD08DA24 CRC64;
Q SEQUENCE

Query Match 19.6%; Score 38; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100 SMDLGPANTKCCNQLDVCYDTGANKYRCDAKPRWCL 137
100 SMDLGPANTKCCNQLDVCYDTGANKYRCDAKPRWCL 137

RESULT 3
ID ADE41 STANDARD; PRT; 214 AA.
AC P11826;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenain (EC 3.4.22.39) (Endoprotease) (Late L3 23 kDa protein).
OS Human adenovirus type 41.
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10524;
[1]
SEQUENCE FROM N.A.
MEDLINE=88160034; PubMed=3279700;
Vos H.L., der Lee F.M., Reenst A.M.C.B., van Loon A.E.,
Sussenbach J.S.;
"The genes encoding the DNA binding protein and the 23K protease of
adenovirus types 40 and 41";
Virology 163:1-10(1988).
[2]
SEQUENCE OF 1-198 FROM N.A.
STRAIN=Tak;
RC Toogood C.I.A., Murali R., Burnett M., Hay R.T.;
Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: THIOLE PROTEASE CLEAVING SPECIFIC GLY-ALA PEPTIDES IN A
NUMBER OF VIRAL PRECURSOR PROTEINS (TERMINAL, IIA, VI, VII, VIII,
IIA AND MU) WHICH ARE REQUIRED FOR VIRION MATURATION. ALSO CLEAVES
HOST CELLS CYTOSKELETAL KERATINS K7 AND K18.
-1- CATALYTIC ACTIVITY: Cleaves proteins of the adenovirus and its
host cell at two consensus sites: -Yaa-Xaa-Gly-Gly-|-Xaa- and
-Yaa-Xaa-Gly-Xaa-|-Gly- (in which Yaa is Met, Ile or Leu, and Xaa
is any amino acid).
-1- SIMILARITY: Belongs to peptidase family C5.

EMBL; M21163; AAA2462.1; -;
EMBL; X51783; CAA36080.1; -;
PIR; E28645; W2AD41.
HSSP; P03252; 1AVP.
MEROPS; C05.001; -;
InterPro; IPR000855; Peptidase C5.
Pfam; PF00770; Peptidase C5; 1.
PRINTS; PR00703; ADENOPTASE.
ProDom; P003705; Peptidase C5; 1.
Kw ProbDom; P003705; Peptidase; Late protein; Autocatalytic cleavage.
FT Adenain (EC 3.4.22.39) (Endoprotease) (Late L3 23 kDa protein).
FT SITE 46 47 CLEAVAGE (AUTO-) (POTENTIAL).
FT ACT_SITE 54 54 BY SIMILARITY.
FT ACT_SITE 71 71 BY SIMILARITY.
FT ACT_SITE 122 122 BY SIMILARITY.

SQ SEQUENCE 214 AA; 24482 MW; 66602CBC786D2371 CRC64;

Query Match 4.1%; Score 8; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 GCGSYFLG 94
DB 16 GCGSYFLG 23

RESULT 4

RLA2 YEAST STANDARD; PRT; 106 AA.
AC P05319;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60S acidic ribosomal protein P2-alpha (A2) (L44) (L12E1B).
GN RPP2A OR RPLA2 OR L12E1B OR RPA2 OR RPL44 OR YOL039W.
OS Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
[1]
SEQUENCE FROM N.A.
STRAIN=IFO 40028;
RX MEDLINE=88233944; PubMed=3287329;
RA Mitsui K., Tsurugi K.;
RT "cDNA and deduced amino acid sequence of acidic ribosomal protein A2
from Saccharomyces cerevisiae";
RL Nucleic Acids Res. 16:3575-3575(1988).
[2]
SEQUENCE FROM N.A.
MEDLINE=88243786; PubMed=2837476;
RA Remacha M., Saenz-Robles M.T., Vilella M.D., Ballesta J.P.G.;
RT "Independent genes coding for three acidic proteins of the large
ribosomal subunit from Saccharomyces cerevisiae";
RL J. Biol. Chem. 263:9094-9101(1988).
[3]
SEQUENCE FROM N.A.
STRAIN=SR26-12C;
RX MEDLINE=90130289; PubMed=2404943;
RA Newton C.H., Shimm L.C., Yee J., Dennis P.P.;
RT "A family of genes encode the multiple forms of the Saccharomycetes
cerevisiae ribosomal proteins equivalent to the Escherichia coli L12
protein and a single form of the L10-equivalent ribosomal protein";
RL J. Bacteriol. 172:579-588(1990).
[4]
SEQUENCE FROM N.A.
RA Ansoorge W., Benes V., Rechmann S., Schwager C., Teodoru C.,
Voss H., Wiemann S.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RA Habbig B., Hattenhorst U., Hollenberg C.P., Ramezani Rad M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Plays an important role in the elongation step of
protein synthesis.
-1- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
-1- PTM: Phosphorylated (By similarity).
-1- MISCELLANEOUS: Yeasts contain 4 individual small ribosomal A
proteins (RPA) which can be classified into two couples of similar
but not identical sequences. Each couple is distinctively related to
one of the two A proteins present in multicellular organisms.
-1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

16-OCT-2001 (Rel. 40, Last annotation update)
60S acidic ribosomal protein P2-beta (L45) (YPA1) (L12E1A).
RPP2B OR RPLA4 OR L12E1A OR RPL45 OR YDR382W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
[1]
SEQUENCE FROM N.A.
MEDLINE=88243786; PubMed=2837476;
Remacha M., Saenz-Robles M.T., Vilella M.D., Ballesta J.P.G.;
"Independent genes coding for three acidic proteins of the large
ribosomal subunit from Saccharomyces cerevisiae";
J. Biol. Chem. 263:9094-9101(1988).
[2]
SEQUENCE FROM N.A.
STRAIN=SR26-12C;
MEDLINE=90130289; PubMed=2404943;
Newton C.H., Shimmin L.C., Yee J., Dennis P.P.;
"A family of genes encode the multiple forms of the Saccharomyces
cerevisiae ribosomal proteins equivalent to the Escherichia coli L12
protein and a single form of the L10-equivalent ribosomal protein";
J. Bacteriol. 172:579-588(1990).
[3]
SEQUENCE FROM N.A.
STRAIN=S288C / A972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevisan E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
Wilson R., Waterston R.;
Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE.
MEDLINE=82069169; PubMed=7030402;
Itoh T.;
"Primary structure of an acidic ribosomal protein YPA1 from
Saccharomyces cerevisiae. Isolation and characterization of peptides
and the complete amino acid sequence";
Biochim. Biophys. Acta 671:16-24(1981).
CC
-!- FUNCTION: Plays an important role in the elongation step of
protein synthesis.
CC
-!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC
-!- PTM: Phosphorylated (By similarity).
CC
-!- MISCELLANEOUS: Yeasts contain 4 individual small ribosomal A
proteins (RPA) which can be classified into two couples of similar
but not identical sequences. Each couple is distinctly related to
one of the two A proteins present in multicellular organisms.
CC
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC

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or send an email to license@isb-sib.ch).
CC

CC EMBL; J03761; AAA34972.1; --
CC EMBL; M26505; AAA34732.1; --
CC EMBL; U28373; AAB64818.1; --
CC EMBL; U32274; AAB64824.1; --
CC PIR; A35109; R5BYA1.
CC GeneOnline; 140874; --
CC SGD; S0002790; RPP2B.
CC InterPro; IPR001813; Ribosomal 60S.
CC Pfam; PF00428; 60S_Ribosomal; 1.
CC Ribosomal protein; Phosphorylation; Multigene family.
CC CONFLICT 75 78 AAGA -> GPAS (IN REF. 4).
CC CONFLICT 86 87 DA -> GD (IN REF. 4).
CC CONFLICT 89 89 E -> A (IN REF. 4).
CC

SQ SEQUENCE 110 AA; 11050 MW; EC45406CB5F199F4 CRC64;
Query Match 3.6%; Score 7; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 AEEKEE 193
DB 88 AEEKEE 94
RESULT 8
RLA4 CLAHE STANDARD; PRT; 111 AA.
AC P42039;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 60S acidic ribosomal protein P2 (Minor allergen Cla h 4) (Cla h IV).
GN CLA4.
OS Cladosporium herbarum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis;
OC Mycosphaerellaceae; Davidiella.
OC NCBI_TaxID=29918;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=280202-Berlin;
EX MEDLINE=95206305; PubMed=7898496;
RA Achatz G., Oberkofler H., Lechenauer E., Simon B., Unger A.,
Kandler D., Ebner C., Prillinger H., Kraft D., Breitenbach M.;
"Molecular cloning of major and minor allergens of Alternaria
alternata and Cladosporium herbarum";
Mol. Immunol. 32:213-227(1995).
RN [2]
RP REVISIONS TO 13; 38-41 AND 93.
RA Simon-Nobbe B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in the elongation step of
protein synthesis.
CC
-!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC
-!- PTM: Phosphorylated (By similarity).
CC
-!- ALLERGEN: Causes an allergic reaction in human.
CC
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC
-!- CAUTION: Two distinct proteins have been termed allergen
Cla h 4.
CC

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CC

CC EMBL; X78223; CAA55067.2; --
CC InterPro; IPR001813; Ribosomal 60S.
CC Pfam; PF00428; 60S_Ribosomal; 1.
CC Ribosomal protein; Phosphorylation; Multigene family; Allergen.
CC KW
CC SEQUENCE 111 AA; 11105 MW; C7B45C6AD997B76A CRC64;
SQ
Query Match 3.6%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 AEEKEE 193
DB 94 AEEKEE 100
RESULT 9
TD53_HUMAN STANDARD; PRT; 204 AA.
ID TD53_HUMAN

```

C Q16890;
T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
T E Tumor protein D53 (hd53) (D52-like 1).
N TP52L1.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
C NCBI_TaxID=9606;
N [1]
C TISSUE=Breast carcinoma;
P MEDLINE=97001154; PubMed=8812487;
X Byrne J.A., Mattei M.-G., Basset P.;
A "Definition of the tumor protein D52 (TPD52) gene family through
T cloning of D52 homologues in human (hd53) and mouse (md52).";
T Genomics 35:523-532(1996).
L [2]
C SEQUENCE FROM N.A.
P INTERACTIONS.
X MEDLINE=98143307; PubMed=9484778;
A Byrne J.A., Nourae C.R., Basset P., Gunning P.;
R "Identification of homo- and heteromeric interactions between members
T of the breast carcinoma-associated D52 protein family using the yeast
T two-hybrid system";
R Oncogene 16:873-881(1998).
L NCBI_TaxID=10090;
C -!- SUBUNIT: Forms homodimer or heterodimer with other members of the
C family.
C -!- SIMILARITY: Belongs to the TPD52 family.
C -----
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C or send an email to license@isb-sib.ch).
C -----
C EMBL; U44427; AAB40894.1; -
C MGI; U44428; AAB40895.1; -
C Genew; HGNC:12006; TPD52L1.
C MIM: 604069; -
C InterPro; IPR007327; TPD52.
C Pfam; PF04201; TPD52; 1.
C Coiled coil. 22 73 COILED COIL (POTENTIAL).
C DOMAIN SEQUENCE 204 AA; 22449 MW; 6B3C336D5C0653C9 CRC64;
C QUERY MATCH 3.6%; Score 7; DB 1; Length 204;
C Best Local Similarity 100.0%; Pred. No. 14;
C Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C -----
C QY 188 EEEKEEL 194
C DB 33 EEEKEEL 39
C -----
C RESULT 10
C TPD53 MOUSE STANDARD; PRT; 204 AA.
C AC 054618;
C DT 16-OCT-2001 (Rel. 40, Created)
C DT 16-OCT-2001 (Rel. 40, Last sequence update)
C DT 16-OCT-2001 (Rel. 40, Last annotation update)
C DE Tumor protein D53 (md53) (D52-like 1).
C GN TP52L1.
C OS Mus musculus (Mouse).
C OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
C OX NCBI_TaxID=10090;
C RN [1]
C FT SEQUENCE FROM N.A.
C MEDLINE=97001154; PubMed=8812487;
C -----
C Query Match 3.6%; Score 7; DB 1; Length 204;
C Best Local Similarity 100.0%; Pred. No. 14;
C Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C -----
C QY 188 EEEKEEL 194
C DB 33 EEEKEEL 39
C -----
C RESULT 11
C TPD53 CHICK STANDARD; PRT; 210 AA.
C AC Q918F4;
C DT 16-OCT-2001 (Rel. 40, Created)
C DT 16-OCT-2001 (Rel. 40, Last sequence update)
C DT 16-OCT-2001 (Rel. 40, Last annotation update)
C DE Tumor protein D53 homolog.
C GN TP52L1.
C OS Gallus gallus (Chicken).
C OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
C OC Gallus.
C OX NCBI_TaxID=9031;
C RN [1]
C FT SEQUENCE FROM N.A.
C Proux V.A., Calothy G., Marx M.;
C Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
C -!- SUBUNIT: Forms homodimer or heterodimer with other members of the
C family (By similarity).
C -!- SIMILARITY: Belongs to the TPD52 family.
C -----
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C or send an email to license@isb-sib.ch).
C -----
C EMBL; AY004870; AAF87084.1; -
C InterPro; IPR007327; TPD52.
C Pfam; PF04201; TPD52; 1.
C Coiled coil. 22 73 COILED COIL (POTENTIAL).
C DOMAIN SEQUENCE 210 AA; 23253 MW; 73AFD4255165A5A6 CRC64;
C QUERY MATCH 3.6%; Score 7; DB 1; Length 210;
C Best Local Similarity 100.0%; Pred. No. 15;
C Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C -----

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OX NCBI_TaxID=2190;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Sadow P.W., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Frazer C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC
CC -!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
CC E.coli protein L10.
CC -!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
CC
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CC
CC -----
CC EMBL; U67500; AAB98499.1; -
CC TIGR; M70509; -
CC HAMAP; MF_00280; -; 1
CC InterPro; IPR001790; Ribosomal_L10.
CC Pfam; PF00466; Ribosomal_L10; 1.
CC Ribosomal protein; Complete proteome.
CC SEQUENCE 338 AA; 36751 MW; 63A6AFD357E3052D CRC64;
SQ
Query Match 3.6%; Score 7; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 ABEKEEE 193
DB 311 ABEKEEE 317
RESULT 14
MSME STRMU STANDARD; PRT; 420 AA.
ID Q00749; 1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DE Multiple sugar-binding protein precursor.
DE MSME OR SMU-878.
GN Streptococcus mutans.
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1309;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Ingbritt;
RX MEDLINE=92165821; PubMed=1537846;
RA Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L.,
RA Ferretti J.J.;
RT "A binding protein-dependent transport system in Streptococcus mutans
RT responsible for multiple sugar metabolism."
RL J. Biol. Chem. 267:4631-4637(1992).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,

```

RL Nature 323:461-464 (1986).
 CC -!- FUNCTION: Removes residual C-terminal Arg or Lys remaining after
 CC initial endoprotease cleavage during prohormone processing.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysine (or L-arginine) + H(2)O =
 CC peptide + L-lysine (or L-arginine).
 CC -!- SUBCELLULAR LOCATION: Secretory granules of pancreatic islets,
 CC adrenal gland, pituitary and brain.
 CC -!- SIMILARITY: Belongs to peptidase family M14.
 CC
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 CC
 CC EMBL; X04411; CAA27999.1; -.
 CC PIR; A24327; A24327.
 CC MEROPS; M14.005; -.
 CC InterPro; IPR008969; Carboxypeptidase_M14.
 CC InterPro; IPR008934; Peptidase_M14.
 CC InterPro; IPR008575; Peptidase_M14B.
 CC Pfam; PF05885; DUF857; 1.
 CC Pfam; PF00246; Zn_carboxypept; 1.
 CC PRINTS; PR00765; CRBOXYPEPTASE.
 CC SMART; SM00631; Zn_pept; 1.
 CC PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
 CC PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
 CC KX Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Glycoprotein.
 CC FT METAL 72 75 75
 CC FT METAL 206 206
 CC FT ACT SITE 300 300
 CC FT CARBOHYD 97 97
 CC FT CARBOHYD 348 348
 CC FT SEQUENCE 434 AA; 49205 MW; E1E848FE5139DBED CRC64;
 CC
 CC Query Match 3.6%; Score 7; DB 1; Length 434;
 CC Best Local Similarity 100.0%; Pred. No. 27;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 188 EEEKEEL 194
 CC Db 415 EEEKEEL 421

Search completed: May 17, 2004, 10:51:51
 Job time : 48 secs

Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
 "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
 pathogen.";
 Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
 CC -!- FUNCTION: Involved in a binding protein-dependent transport system
 CC responsible for the uptake of melibiose, raffinose and
 CC isomaltotriose.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- INDUCTION: By raffinose.
 CC -!- SIMILARITY: Belongs to the bacterial extracellular solute-binding
 CC protein family 1.
 CC
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 CC
 CC EMBL; M77351; AAA26934.1; -.
 CC EMBL; AE014929; AAN58593.1; -.
 CC PIR; B42400; B42400.
 CC InterPro; IPR000437; Prok lipoprot_S.
 CC InterPro; IPR006059; SBP_bac1.
 CC InterPro; IPR006061; SBP_dom1.
 CC Pfam; PF01547; SBP_bac1; 1.
 CC PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 CC PROSITE; PS01037; SBP_BACTERIAL_1; 1.
 CC Transprot; Sugar transport; Lipoprotein; Membrane; Signal;
 CC Complete proteome; Palmitate.
 CC SIGNAL 1 22
 CC CHAIN 23 420 MULTIPLE SUGAR-BINDING PROTEIN.
 CC LIPID 23 23 N-palmitoyl cysteine (Probable).
 CC LIPID 23 23 S-diacylglycerol cysteine (Probable).
 CC CONFLICT 27 28 KA -> NG (IN REF. 1).
 CC CONFLICT 33 33 E -> D (IN REF. 1).
 CC CONFLICT 277 287 ALPAKQDQPK -> PCOLLNNKIPN (IN REF. 1).
 CC CONFLICT 372 372 D -> H (IN REF. 1).
 CC CONFLICT 388 388 F -> L (IN REF. 1).
 CC SEQUENCE 420 AA; 47087 MW; FA7CF7AECG3DEFA7 CRC64;
 CC
 CC Query Match 3.6%; Score 7; DB 1; Length 420;
 CC Best Local Similarity 100.0%; Pred. No. 26;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 93 LGLKVPE 99
 CC Db 158 LGLKVPE 164

RESULT 15
 CBPH BOVIN STANDARD; PRT; 434 AA.
 ID CBPH BOVIN STANDARD; PRT; 434 AA.
 AC P04836;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carboxypeptidase H (EC 3.4.17.10) (CPH) (Carboxypeptidase E) (CPE)
 DE (Enkephalin convertase) (Prohormone processing carboxypeptidase).
 GN CPE.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CC NCBI TaxID=9913;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=87014809; PubMed=3020433;
 CC Fricker L.D., Evans C.J., Esch F.S., Herbert E.;
 CC "Cloning and sequence analysis of cDNA for bovine carboxypeptidase
 CC E.";

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MM protein - protein search, using sw model

Run on: May 17, 2004, 10:48:10 ; Search time 45 Seconds
(without alignments)
1360.234 Million cell updates/sec

Title: US-10-621-401-145
Perfect score: 194
Sequence: 1 MLAGFLVLSLGGGLAQ.....PFMNSQRAACICAEKEEL 194

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 38 | 19.6 | 195 | 11 | Q8VC81 |
| 2 | 13 | 6.7 | 180 | 13 | Q7ZTY1 |
| 3 | 8 | 4.1 | 321 | 16 | Q8XGL7 |
| 4 | 8 | 4.1 | 484 | 16 | Q8B38 |
| 5 | 8 | 4.1 | 489 | 16 | Q9L004 |
| 6 | 8 | 4.1 | 497 | 16 | Q7WL74 |
| 7 | 8 | 4.1 | 497 | 16 | Q7W7T4 |
| 8 | 8 | 4.1 | 497 | 16 | Q7VWF4 |
| 9 | 8 | 4.1 | 528 | 10 | Q9C6J7 |
| 10 | 8 | 4.1 | 603 | 16 | Q899H3 |
| 11 | 8 | 4.1 | 637 | 3 | Q9Y815 |
| 12 | 8 | 4.1 | 768 | 10 | Q9C6J6 |
| 13 | 8 | 4.1 | 5035 | 11 | Q80X16 |
| 14 | 7 | 3.6 | 49 | 16 | Q984N0 |
| 15 | 7 | 3.6 | 63 | 16 | Q8YMR5 |
| 16 | 7 | 3.6 | 75 | 17 | Q97ZP8 |

| | | | | | |
|----|-----|-----|----|--------|---------------------|
| 17 | 3.6 | 75 | 17 | Q97XE7 | Q97xe7 sulfolobus |
| 18 | 3.6 | 88 | 2 | Q9L9D8 | Q9L9d8 bordetella |
| 19 | 3.6 | 88 | 16 | Q84CR2 | Q84cr2 bordetella |
| 20 | 3.6 | 91 | 16 | Q7WLW2 | Q7wlw2 bordetella |
| 21 | 3.6 | 91 | 16 | Q7W8A3 | Q7w8a3 bordetella |
| 22 | 3.6 | 103 | 4 | Q9NNZ6 | Q9nnz6 homo sapien |
| 23 | 3.6 | 106 | 3 | Q9HFQ7 | Q9hfg7 candida alb |
| 24 | 3.6 | 106 | 3 | Q9A0L8 | Q9a0l8 candida alb |
| 25 | 3.6 | 110 | 2 | Q939G1 | Q939g1 pseudomonas |
| 26 | 3.6 | 111 | 3 | Q9HFQ4 | Q9hfg4 candida alb |
| 27 | 3.6 | 124 | 16 | Q82Q59 | Q82q59 streptomyce |
| 28 | 3.6 | 131 | 4 | Q9C054 | Q9c054 homo sapien |
| 29 | 3.6 | 133 | 10 | Q7XY30 | Q7xy30 griffithsia |
| 30 | 3.6 | 144 | 4 | Q9BU06 | Q9buz6 homo sapien |
| 31 | 3.6 | 144 | 4 | Q43397 | Q43397 homo sapien |
| 32 | 3.6 | 158 | 16 | Q92P52 | Q92p52 rhizobium m |
| 33 | 3.6 | 168 | 16 | Q8XQ01 | Q8xq01 ralstonia s |
| 34 | 3.6 | 174 | 16 | Q83AR0 | Q83ar0 coxiella bu |
| 35 | 3.6 | 182 | 12 | Q7T4F6 | Q7t4f6 pike fry-li |
| 36 | 3.6 | 182 | 12 | Q7T4F5 | Q7t4f5 pike fry-li |
| 37 | 3.6 | 182 | 12 | Q7T4F4 | Q7t4f4 pike fry-li |
| 38 | 3.6 | 182 | 12 | Q7T4F3 | Q7t4f3 pike fry-li |
| 39 | 3.6 | 182 | 12 | Q7T4F2 | Q7t4f2 pike fry-li |
| 40 | 3.6 | 182 | 12 | Q7T4E4 | Q7t4e4 pike fry-li |
| 41 | 3.6 | 182 | 12 | Q7T4E3 | Q7t4e3 pike fry-li |
| 42 | 3.6 | 182 | 12 | Q7T4E2 | Q7t4e2 pike fry-li |
| 43 | 3.6 | 182 | 12 | Q7T4E1 | Q7t4e1 pike fry-li |
| 44 | 3.6 | 182 | 12 | Q7T4E0 | Q7t4e0 pike fry-li |
| 45 | 3.6 | 182 | 12 | Q7T4D9 | Q7t4d9 pike fry-li |
| 46 | 3.6 | 182 | 12 | Q7T4D8 | Q7t4d8 pike fry-li |
| 47 | 3.6 | 182 | 12 | Q7T4D7 | Q7t4d7 pike fry-li |
| 48 | 3.6 | 182 | 12 | Q7T4D6 | Q7t4d6 pike fry-li |
| 49 | 3.6 | 182 | 12 | Q7T4D5 | Q7t4d5 pike fry-li |
| 50 | 3.6 | 182 | 12 | Q7T4D4 | Q7t4d4 pike fry-li |
| 51 | 3.6 | 182 | 12 | Q7T4D3 | Q7t4d3 pike fry-li |
| 52 | 3.6 | 182 | 12 | Q7T4D2 | Q7t4d2 pike fry-li |
| 53 | 3.6 | 182 | 12 | Q7T4D1 | Q7t4d1 pike fry-li |
| 54 | 3.6 | 182 | 12 | Q7T4D0 | Q7t4d0 pike fry-li |
| 55 | 3.6 | 191 | 10 | Q82809 | Q82809 arabidopsis |
| 56 | 3.6 | 191 | 10 | Q8LDX1 | Q8ldx1 arabidopsis |
| 57 | 3.6 | 191 | 10 | Q04154 | Q04154 arabidopsis |
| 58 | 3.6 | 212 | 12 | Q91TR8 | Q91tr8 tupaia herp |
| 59 | 3.6 | 241 | 2 | Q51308 | Q51308 nitrosospi |
| 60 | 3.6 | 243 | 4 | Q86X76 | Q86x76 homo sapien |
| 61 | 3.6 | 244 | 16 | Q836D4 | Q836d4 enterococcu |
| 62 | 3.6 | 255 | 2 | Q54889 | Q54889 serratia pr |
| 63 | 3.6 | 258 | 3 | Q93871 | Q93871 verticillu |
| 64 | 3.6 | 260 | 16 | Q82HP0 | Q82hp0 streptomyce |
| 65 | 3.6 | 270 | 17 | Q8PWH1 | Q8pwh1 methanosarc |
| 66 | 3.6 | 277 | 10 | Q8S253 | Q8s253 oryza sativ |
| 67 | 3.6 | 287 | 16 | Q8BL04 | Q8dl04 yersinia pe |
| 68 | 3.6 | 288 | 13 | Q918G0 | Q918g0 xenopus lae |
| 69 | 3.6 | 293 | 16 | Q7UJF6 | Q7ujf6 rhodospirell |
| 70 | 3.6 | 298 | 5 | Q20193 | Q20193 caenorhabdi |
| 71 | 3.6 | 300 | 5 | Q9N8B3 | Q9n8b3 trypanosoma |
| 72 | 3.6 | 303 | 2 | Q9R3A7 | Q9r3a7 escherichia |
| 73 | 3.6 | 304 | 2 | Q53792 | Q53792 streptomyce |
| 74 | 3.6 | 309 | 16 | Q82VR6 | Q82vr6 nitrosomona |
| 75 | 3.6 | 312 | 16 | Q8PA20 | Q8paz0 xanthomonas |
| 76 | 3.6 | 314 | 3 | Q9C3Z6 | Q9c3z6 podospora a |
| 77 | 3.6 | 317 | 16 | Q8UBZ1 | Q8ubz1 agrobacteri |
| 78 | 3.6 | 320 | 2 | Q8RKT9 | Q8rkt9 serratia ma |
| 79 | 3.6 | 320 | 2 | Q9X9D8 | Q9x9d8 serratia sp |
| 80 | 3.6 | 320 | 16 | Q8ZD83 | Q8zdz3 yersinia pe |
| 81 | 3.6 | 324 | 2 | Q85477 | Q85477 yersinia en |
| 82 | 3.6 | 326 | 2 | Q68878 | Q68878 pseudomonas |
| 83 | 3.6 | 327 | 4 | Q76091 | Q76091 homo sapien |
| 84 | 3.6 | 327 | 16 | Q9HV91 | Q9hv91 pseudomonas |
| 85 | 3.6 | 337 | 2 | Q8GL33 | Q8gl33 borrelia bu |
| 86 | 3.6 | 343 | 2 | Q9S035 | Q9s035 borrelia bu |
| 87 | 3.6 | 348 | 13 | Q7SZ21 | Q7sz21 xenopus lae |
| 88 | 3.6 | 363 | 5 | Q9N4W7 | Q9n4w7 caenorhabdi |
| 89 | 3.6 | 380 | 17 | Q8Z2C8 | Q8zzc8 pyrobaculum |

| | | | | | | | | | | | | | |
|-----|---|-----|------|----|---------|---------------------|-----|---|-----|------|----|--------|---------------------|
| 90 | 7 | 3.6 | 388 | 5 | Q9N888 | Q9N888 plasmodium | 163 | 7 | 3.6 | 1231 | 5 | Q24098 | Q24098 drosophila |
| 91 | 7 | 3.6 | 395 | 16 | Q8PIL0 | Q8PIL0 xanthomonas | 164 | 7 | 3.6 | 1294 | 16 | Q8PKH5 | Q8PKH5 xanthomonas |
| 92 | 7 | 3.6 | 398 | 16 | Q8P791 | Q8P791 xanthomonas | 165 | 7 | 3.6 | 1305 | 3 | Q9P424 | Q9P424 ajellomyces |
| 93 | 7 | 3.6 | 412 | 12 | Q9QH54 | Q9QH54 gallid herp | 166 | 7 | 3.6 | 1318 | 16 | Q7UG24 | Q7UG24 rhodopirell |
| 94 | 7 | 3.6 | 418 | 10 | Q64517 | Q64517 arabidopsis | 167 | 7 | 3.6 | 1381 | 11 | Q8CGE9 | Q8CGE9 mus musculus |
| 95 | 7 | 3.6 | 418 | 10 | Q7XB11 | Q7XB11 arabidopsis | 168 | 7 | 3.6 | 1548 | 10 | Q85531 | Q85531 arabidopsis |
| 96 | 7 | 3.6 | 419 | 16 | Q9TNW2 | Q9TNW2 streptococc | 169 | 7 | 3.6 | 1846 | 4 | Q8GYS8 | Q8GYS8 homo sapien |
| 97 | 7 | 3.6 | 419 | 16 | Q8DNH8 | Q8DNH8 streptococc | 170 | 7 | 3.6 | 2109 | 5 | Q8IAS7 | Q8IAS7 plasmodium |
| 98 | 7 | 3.6 | 442 | 4 | Q8N7F2 | Q8N7F2 homo sapien | 171 | 7 | 3.6 | 2515 | 5 | Q24551 | Q24551 drosophila |
| 99 | 7 | 3.6 | 448 | 16 | Q9KFP87 | Q9KFP87 bacillus ha | 172 | 7 | 3.6 | 2731 | 5 | Q9VNU6 | Q9VNU6 drosophila |
| 100 | 7 | 3.6 | 451 | 16 | Q5O870 | Q5O870 borrelia bu | 173 | 7 | 3.6 | 2731 | 5 | Q61307 | Q61307 drosophila |
| 101 | 7 | 3.6 | 460 | 17 | Q58649 | Q58649 pyrococcus | 174 | 7 | 3.6 | 2731 | 5 | Q61307 | Q61307 drosophila |
| 102 | 7 | 3.6 | 464 | 17 | Q9U2B9 | Q9U2B9 pyrococcus | 175 | 7 | 3.6 | 4163 | 2 | Q9LAE6 | Q9LAE6 dictyostell |
| 103 | 7 | 3.6 | 465 | 17 | Q85724 | Q85724 homo sapien | 176 | 7 | 3.6 | 4730 | 5 | Q8TI28 | Q8TI28 rhodococcus |
| 104 | 7 | 3.6 | 489 | 2 | Q9H925 | Q9H925 homo sapien | 177 | 6 | 3.1 | 21 | 21 | Q9R5U9 | Q9R5U9 rhodococcus |
| 105 | 7 | 3.6 | 502 | 4 | Q9CAD4 | Q9CAD4 arabidopsis | 178 | 6 | 3.1 | 28 | 2 | Q50102 | Q50102 mycobacteri |
| 106 | 7 | 3.6 | 519 | 10 | Q9ZAL7 | Q9ZAL7 rattus norv | 179 | 6 | 3.1 | 31 | 11 | Q8CGM7 | Q8CGM7 mus musculu |
| 107 | 7 | 3.6 | 523 | 2 | Q54200 | Q54200 streptomyce | 180 | 6 | 3.1 | 49 | 9 | Q8H9K8 | Q8H9K8 vibrio harv |
| 108 | 7 | 3.6 | 539 | 11 | Q8ZLU7 | Q8ZLU7 rattus norv | 181 | 6 | 3.1 | 50 | 12 | Q8V270 | Q8V270 human herpe |
| 109 | 7 | 3.6 | 540 | 10 | Q8LCK4 | Q8LCK4 arabidopsis | 182 | 6 | 3.1 | 53 | 2 | Q93A11 | Q93A11 thibacillu |
| 110 | 7 | 3.6 | 540 | 10 | Q8W469 | Q8W469 arabidopsis | 183 | 6 | 3.1 | 54 | 16 | Q7UYJ1 | Q7UYJ1 rhodopirell |
| 111 | 7 | 3.6 | 547 | 10 | Q8SFV1 | Q8SFV1 arabidopsis | 184 | 6 | 3.1 | 57 | 17 | Q8PZF5 | Q8PZF5 methanosarc |
| 112 | 7 | 3.6 | 548 | 16 | Q8FOP9 | Q8FOP9 corynebacte | 185 | 6 | 3.1 | 59 | 9 | Q8MCE5 | Q8MCE5 lactococcus |
| 113 | 7 | 3.6 | 564 | 5 | Q9V369 | Q9V369 drosophila | 186 | 6 | 3.1 | 60 | 10 | Q9LUD9 | Q9LUD9 arabidopsis |
| 114 | 7 | 3.6 | 619 | 4 | Q73453 | Q73453 homo sapien | 187 | 6 | 3.1 | 60 | 10 | Q9LUD9 | Q9LUD9 mus musculu |
| 115 | 7 | 3.6 | 632 | 10 | Q9C6K1 | Q9C6K1 arabidopsis | 188 | 6 | 3.1 | 60 | 11 | Q9CSJ9 | Q9CSJ9 mus musculu |
| 116 | 7 | 3.6 | 649 | 4 | Q86PL7 | Q86PL7 homo sapien | 189 | 6 | 3.1 | 62 | 16 | Q9CG40 | Q9CG40 lactococcus |
| 117 | 7 | 3.6 | 650 | 4 | Q8IYX9 | Q8IYX9 homo sapien | 190 | 6 | 3.1 | 62 | 16 | Q9CG40 | Q9CG40 lactococcus |
| 118 | 7 | 3.6 | 652 | 4 | Q8B357 | Q8B357 homo sapien | 191 | 6 | 3.1 | 67 | 16 | Q7UEY9 | Q7UEY9 rhodopirell |
| 119 | 7 | 3.6 | 653 | 6 | Q95L97 | Q95L97 felis silve | 192 | 6 | 3.1 | 68 | 16 | Q8R7Q8 | Q8R7Q8 thermoaer |
| 120 | 7 | 3.6 | 666 | 10 | Q8RXC3 | Q8RXC3 arabidopsis | 193 | 6 | 3.1 | 70 | 16 | Q8Q9Q3 | Q8Q9Q3 bradyrhizob |
| 121 | 7 | 3.6 | 677 | 16 | Q9KAS2 | Q9KAS2 bacillus ha | 194 | 6 | 3.1 | 71 | 5 | Q93186 | Q93186 caenorhabdi |
| 122 | 7 | 3.6 | 678 | 2 | Q9KX14 | Q9KX14 mycobacteri | 195 | 6 | 3.1 | 73 | 5 | Q8T844 | Q8T844 dictyosteli |
| 123 | 7 | 3.6 | 678 | 8 | Q7YJX9 | Q7YJX9 calycanthus | 196 | 6 | 3.1 | 74 | 7 | Q79637 | Q79637 oncorhynch |
| 124 | 7 | 3.6 | 687 | 2 | Q8KU02 | Q8KU02 listeria mo | 197 | 6 | 3.1 | 75 | 11 | Q8VEI7 | Q8VEI7 mus musculu |
| 125 | 7 | 3.6 | 722 | 13 | Q9W6K6 | Q9W6K6 salmo salar | 198 | 6 | 3.1 | 75 | 12 | O57140 | O57140 human herpe |
| 126 | 7 | 3.6 | 723 | 11 | Q9D677 | Q9D677 mus musculu | 199 | 6 | 3.1 | 76 | 7 | Q95IW9 | Q95IW9 oncorhynch |
| 127 | 7 | 3.6 | 725 | 4 | Q86WM9 | Q86WM9 homo sapien | 200 | 6 | 3.1 | 76 | 7 | Q95IW9 | Q95IW9 human herpe |
| 128 | 7 | 3.6 | 732 | 4 | Q9H7P8 | Q9H7P8 homo sapien | 201 | 6 | 3.1 | 79 | 12 | Q96895 | Q96895 human herpe |
| 129 | 7 | 3.6 | 734 | 16 | Q8XN26 | Q8XN26 clostridium | 202 | 6 | 3.1 | 80 | 17 | Q9HHP8 | Q9HHP8 halobacteri |
| 130 | 7 | 3.6 | 736 | 2 | P77038 | P77038 escherichia | 203 | 6 | 3.1 | 82 | 9 | Q853Y6 | Q853Y6 mycobacteri |
| 131 | 7 | 3.6 | 753 | 16 | Q7UHR1 | Q7UHR1 rhodopirell | 204 | 6 | 3.1 | 82 | 16 | Q8PFE2 | Q8PFE2 xanthomonas |
| 132 | 7 | 3.6 | 759 | 4 | Q9NWL3 | Q9NWL3 homo sapien | 205 | 6 | 3.1 | 84 | 16 | Q8UBK9 | Q8UBK9 agrobacteri |
| 133 | 7 | 3.6 | 759 | 4 | Q86CV3 | Q86CV3 homo sapien | 206 | 6 | 3.1 | 86 | 1 | Q8U750 | Q8U750 methanobact |
| 134 | 7 | 3.6 | 771 | 4 | Q96C12 | Q96C12 homo sapien | 207 | 6 | 3.1 | 86 | 5 | Q8T5K9 | Q8T5K9 anopheles g |
| 135 | 7 | 3.6 | 780 | 10 | Q9SAI0 | Q9SAI0 arabidopsis | 208 | 6 | 3.1 | 86 | 6 | Q8HZZ8 | Q8HZZ8 macaca fasc |
| 136 | 7 | 3.6 | 783 | 10 | Q9FVX6 | Q9FVX6 arabidopsis | 209 | 6 | 3.1 | 89 | 10 | Q42367 | Q42367 zea mays (m |
| 137 | 7 | 3.6 | 788 | 4 | Q8TDQ5 | Q8TDQ5 homo sapien | 210 | 6 | 3.1 | 90 | 10 | Q42368 | Q42368 zea mays (m |
| 138 | 7 | 3.6 | 791 | 4 | Q9V4S4 | Q9V4S4 homo sapien | 211 | 6 | 3.1 | 90 | 10 | Q8H4N9 | Q8H4N9 oryza sativ |
| 139 | 7 | 3.6 | 812 | 10 | Q9C6J9 | Q9C6J9 arabidopsis | 212 | 6 | 3.1 | 91 | 16 | Q8ER66 | Q8ER66 oceanobacil |
| 140 | 7 | 3.6 | 816 | 16 | Q9CHS9 | Q9CHS9 lactococcus | 213 | 6 | 3.1 | 92 | 10 | Q9LGG9 | Q9LGG9 oryza sativ |
| 141 | 7 | 3.6 | 822 | 16 | Q8EUA6 | Q8EUA6 mycoplasma | 214 | 6 | 3.1 | 93 | 13 | Q801B3 | Q801B3 latimeria m |
| 142 | 7 | 3.6 | 832 | 10 | Q9SLE5 | Q9SLE5 arabidopsis | 215 | 6 | 3.1 | 94 | 12 | Q8JQM5 | Q8JQM5 human herpe |
| 143 | 7 | 3.6 | 848 | 10 | Q9SCU9 | Q9SCU9 arabidopsis | 216 | 6 | 3.1 | 94 | 12 | Q8JQM5 | Q8JQM5 human herpe |
| 144 | 7 | 3.6 | 851 | 16 | Q9I442 | Q9I442 pseudomonas | 217 | 6 | 3.1 | 95 | 16 | Q8JQJ1 | Q8JQJ1 human herpe |
| 145 | 7 | 3.6 | 879 | 10 | Q82177 | Q82177 arabidopsis | 218 | 6 | 3.1 | 95 | 16 | Q7UUM1 | Q7UUM1 rhodopirell |
| 146 | 7 | 3.6 | 896 | 5 | Q19370 | Q19370 caenorhabdi | 219 | 6 | 3.1 | 96 | 16 | Q8PXP7 | Q8PXP7 methanosarc |
| 147 | 7 | 3.6 | 900 | 10 | Q23454 | Q23454 arabidopsis | 220 | 6 | 3.1 | 96 | 16 | Q82QHO | Q82QHO streptomyce |
| 148 | 7 | 3.6 | 931 | 5 | Q9VVU6 | Q9VVU6 drosophila | 221 | 6 | 3.1 | 97 | 10 | Q04816 | Q04816 sporobolus |
| 149 | 7 | 3.6 | 962 | 10 | Q84KL1 | Q84KL1 cyanidiosch | 222 | 6 | 3.1 | 98 | 13 | Q90XG3 | Q90XG3 gallus gall |
| 150 | 7 | 3.6 | 962 | 16 | Q837Q7 | Q837Q7 enterococcu | 223 | 6 | 3.1 | 98 | 16 | Q7VKK5 | Q7VKK5 haemophilus |
| 151 | 7 | 3.6 | 1041 | 12 | Q9ELF7 | Q9ELF7 meleagrid h | 224 | 6 | 3.1 | 99 | 17 | Q26906 | Q26906 methanobact |
| 152 | 7 | 3.6 | 1041 | 12 | Q9DPQ2 | Q9DPQ2 meleagrid h | 225 | 6 | 3.1 | 99 | 17 | Q9UX03 | Q9UX03 sulfolobus |
| 153 | 7 | 3.6 | 1054 | 5 | Q8IRI2 | Q8IRI2 drosophila | 226 | 6 | 3.1 | 100 | 2 | O52301 | O52301 escherichia |
| 154 | 7 | 3.6 | 1126 | 11 | Q8BHP2 | Q8BHP2 mus musculu | 227 | 6 | 3.1 | 100 | 2 | O52302 | O52302 escherichia |
| 155 | 7 | 3.6 | 1132 | 4 | Q86Y26 | Q86Y26 homo sapien | 228 | 6 | 3.1 | 100 | 16 | Q89AT7 | Q89AT7 buchnera ap |
| 156 | 7 | 3.6 | 1137 | 5 | Q9V649 | Q9V649 drosophila | 229 | 6 | 3.1 | 101 | 11 | Q8BMV6 | Q8BMV6 mus musculu |
| 157 | 7 | 3.6 | 1146 | 5 | Q8MRD5 | Q8MRD5 drosophila | 230 | 6 | 3.1 | 101 | 12 | Q8JMC8 | Q8JMC8 manestra co |
| 158 | 7 | 3.6 | 1200 | 5 | Q9VXE9 | Q9VXE9 drosophila | 231 | 6 | 3.1 | 104 | 17 | Q96Z31 | Q96Z31 sulfolobus |
| 159 | 7 | 3.6 | 1201 | 5 | Q8I952 | Q8I952 anopheles g | 232 | 6 | 3.1 | 107 | 17 | Q8TZJ7 | Q8TZJ7 pyrococcus |
| 160 | 7 | 3.6 | 1217 | 4 | Q86VX4 | Q86VX4 homo sapien | 233 | 6 | 3.1 | 108 | 10 | Q8W332 | Q8W332 oryza sativ |
| 161 | 7 | 3.6 | 1217 | 13 | Q8AWB8 | Q8AWB8 gallus gall | 234 | 6 | 3.1 | 108 | 11 | Q8C6T8 | Q8C6T8 mus musculu |
| 162 | 7 | 3.6 | 1217 | 13 | Q8AW91 | Q8AW91 xenopus lae | 235 | 6 | 3.1 | 109 | 3 | Q8TFM9 | Q8TFM9 fusarium cu |

| | | | | | | | | | | | | | |
|-----|---|-----|-----|----|--------|---------------------|-----|---|-----|-----|----|--------|---------------------|
| 236 | 6 | 3.1 | 109 | 10 | Q8LBM7 | Q8LBM7 arabidopsis | 309 | 6 | 3.1 | 144 | 8 | Q9TJZ2 | Q9TJZ2 arabidopsis |
| 237 | 6 | 3.1 | 110 | 2 | Q8VQR3 | Q8VQR3 escherichia | 310 | 6 | 3.1 | 144 | 16 | Q8YM42 | Q8YM42 anabaena sp |
| 238 | 6 | 3.1 | 110 | 2 | Q8VNS4 | Q8VNS4 escherichia | 311 | 6 | 3.1 | 145 | 11 | Q8CD69 | Q8CD69 mus musculus |
| 239 | 6 | 3.1 | 110 | 9 | Q8O048 | Q8O048 escherichia | 312 | 6 | 3.1 | 146 | 2 | Q9R8B8 | Q9R8B8 pseudomonas |
| 240 | 6 | 3.1 | 110 | 9 | Q8SDK7 | Q8SDK7 staphylococ | 313 | 6 | 3.1 | 146 | 2 | Q9X6F3 | Q9X6F3 pseudomonas |
| 241 | 6 | 3.1 | 110 | 11 | Q8C316 | Q8C316 mus musculus | 314 | 6 | 3.1 | 148 | 10 | Q9M4E1 | Q9M4E1 avena sativ |
| 242 | 6 | 3.1 | 110 | 16 | Q8NQ00 | Q8NQ00 staphylococ | 315 | 6 | 3.1 | 149 | 16 | Q8ZCA9 | Q8ZCA9 yersinia pe |
| 243 | 6 | 3.1 | 110 | 16 | Q7UI77 | Q7UI77 rhodopirell | 316 | 6 | 3.1 | 149 | 17 | Q7UXE1 | Q7UXE1 rhodopirell |
| 244 | 6 | 3.1 | 110 | 17 | Q8HTB3 | Q8HTB3 methanosaarc | 317 | 6 | 3.1 | 149 | 17 | Q8TW19 | Q8TW19 methanopyru |
| 245 | 6 | 3.1 | 111 | 3 | Q8HGV0 | Q8HGV0 aspergillus | 318 | 6 | 3.1 | 150 | 16 | Q8XEN4 | Q8XEN4 salmonella |
| 246 | 6 | 3.1 | 111 | 3 | Q8HG99 | Q8HG99 aspergillus | 319 | 6 | 3.1 | 150 | 16 | Q8ZQI1 | Q8ZQI1 streptomyce |
| 247 | 6 | 3.1 | 111 | 3 | Q8C325 | Q8C325 podospora a | 320 | 6 | 3.1 | 151 | 10 | Q9FGU8 | Q9FGU8 arabidopsis |
| 248 | 6 | 3.1 | 111 | 17 | Q8ZX60 | Q8ZX60 pyrobaculum | 321 | 6 | 3.1 | 151 | 10 | Q8LB92 | Q8LB92 arabidopsis |
| 249 | 6 | 3.1 | 112 | 6 | Q847F8 | Q847F8 oryctolagus | 322 | 6 | 3.1 | 151 | 12 | Q6S866 | Q6S866 barley yell |
| 250 | 6 | 3.1 | 113 | 5 | Q9N1V6 | Q9N1V6 tegula mont | 323 | 6 | 3.1 | 151 | 16 | Q8XD05 | Q8XD05 escherichia |
| 251 | 6 | 3.1 | 113 | 9 | Q9MBP8 | Q9MBP8 staphylococ | 324 | 6 | 3.1 | 152 | 2 | Q8KY49 | Q8KY49 escherichia |
| 252 | 6 | 3.1 | 113 | 16 | Q8D3A4 | Q8D3A4 wigwagwort | 325 | 6 | 3.1 | 152 | 16 | Q8PK72 | Q8PK72 escherichia |
| 253 | 6 | 3.1 | 114 | 10 | Q8LLC1 | Q8LLC1 hordeum vul | 326 | 6 | 3.1 | 152 | 16 | Q8PDX9 | Q8PDX9 escherichia |
| 254 | 6 | 3.1 | 114 | 10 | Q8LUX2 | Q8LUX2 arabidopsis | 327 | 6 | 3.1 | 152 | 16 | Q7VE00 | Q7VE00 prochloroco |
| 255 | 6 | 3.1 | 114 | 16 | Q8PG96 | Q8PG96 xanthomonas | 328 | 6 | 3.1 | 152 | 16 | Q8KQ32 | Q8KQ32 pseudomonas |
| 256 | 6 | 3.1 | 115 | 5 | Q8IFK4 | Q8IFK4 riftia pach | 329 | 6 | 3.1 | 155 | 2 | Q8Q32 | Q8Q32 methanosaarc |
| 257 | 6 | 3.1 | 115 | 11 | Q8CAME | Q8CAME mus musculus | 330 | 6 | 3.1 | 155 | 17 | Q8PVH8 | Q8PVH8 methanosaarc |
| 258 | 6 | 3.1 | 115 | 16 | Q7V2D9 | Q7V2D9 prochloroco | 331 | 6 | 3.1 | 156 | 5 | Q9XTZ7 | Q9XTZ7 caenorhabdi |
| 259 | 6 | 3.1 | 116 | 8 | Q8GS81 | Q8GS81 oryza sativ | 332 | 6 | 3.1 | 157 | 11 | Q8BHZ5 | Q8BHZ5 mus musculus |
| 260 | 6 | 3.1 | 116 | 10 | Q8ETA7 | Q8ETA7 oceanobacil | 333 | 6 | 3.1 | 158 | 10 | Q8G5L9 | Q8G5L9 methylobact |
| 261 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 334 | 6 | 3.1 | 158 | 16 | Q934V0 | Q934V0 oryza sativ |
| 262 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 335 | 6 | 3.1 | 158 | 16 | Q8XS17 | Q8XS17 salmonella |
| 263 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 336 | 6 | 3.1 | 160 | 5 | Q8B8H9 | Q8B8H9 schistosoma |
| 264 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 337 | 6 | 3.1 | 161 | 4 | Q7Z5K0 | Q7Z5K0 homo sapien |
| 265 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 338 | 6 | 3.1 | 161 | 12 | Q8UZD3 | Q8UZD3 cercopithic |
| 266 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 339 | 6 | 3.1 | 162 | 16 | Q8PJ48 | Q8PJ48 xanthomonas |
| 267 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 340 | 6 | 3.1 | 162 | 17 | Q8S548 | Q8S548 pyrococcus |
| 268 | 6 | 3.1 | 117 | 8 | Q8G81 | Q8G81 oryza sativ | 341 | 6 | 3.1 | 162 | 16 | Q8P7U0 | Q8P7U0 xanthomonas |
| 269 | 6 | 3.1 | 118 | 5 | Q8L3S2 | Q8L3S2 plasmodium | 342 | 6 | 3.1 | 163 | 16 | Q94AA2 | Q94AA2 arabidopsis |
| 270 | 6 | 3.1 | 120 | 12 | Q69247 | Q69247 bovine herp | 343 | 6 | 3.1 | 164 | 16 | Q8BNT4 | Q8BNT4 pseudomonas |
| 271 | 6 | 3.1 | 120 | 16 | Q8Z1J8 | Q8Z1J8 salmonella | 344 | 6 | 3.1 | 164 | 16 | Q87XQ0 | Q87XQ0 pseudomonas |
| 272 | 6 | 3.1 | 121 | 10 | Q9SDS0 | Q9SDS0 prunus dulc | 345 | 6 | 3.1 | 165 | 16 | Q9JKE2 | Q9JKE2 mus musculus |
| 273 | 6 | 3.1 | 122 | 2 | Q9P8F2 | Q9P8F2 bacillus su | 346 | 6 | 3.1 | 166 | 11 | Q9WJX0 | Q9WJX0 hepatitis e |
| 274 | 6 | 3.1 | 122 | 16 | Q8R7M0 | Q8R7M0 thermoanaer | 347 | 6 | 3.1 | 168 | 12 | Q9WJX0 | Q9WJX0 hepatitis e |
| 275 | 6 | 3.1 | 123 | 16 | Q8F6E4 | Q8F6E4 leptospira | 348 | 6 | 3.1 | 168 | 16 | Q9CP78 | Q9CP78 pasteurella |
| 276 | 6 | 3.1 | 124 | 16 | Q8BPC1 | Q8BPC1 pseudomonas | 349 | 6 | 3.1 | 168 | 16 | Q9CP78 | Q9CP78 pasteurella |
| 277 | 6 | 3.1 | 124 | 16 | Q8BPC1 | Q8BPC1 pseudomonas | 350 | 6 | 3.1 | 168 | 16 | Q9CP78 | Q9CP78 pasteurella |
| 278 | 6 | 3.1 | 126 | 8 | Q7YBU0 | Q7YBU0 pectinopygu | 351 | 6 | 3.1 | 170 | 16 | Q9Z956 | Q9Z956 chlamydia p |
| 279 | 6 | 3.1 | 126 | 9 | Q9T1F5 | Q9T1F5 lactobacill | 352 | 6 | 3.1 | 171 | 10 | Q9FWH2 | Q9FWH2 arabidopsis |
| 280 | 6 | 3.1 | 126 | 16 | Q8FTD1 | Q8FTD1 corynebacte | 353 | 6 | 3.1 | 171 | 10 | Q9FWH2 | Q9FWH2 arabidopsis |
| 281 | 6 | 3.1 | 126 | 16 | Q8SUU0 | Q8SUU0 encephalito | 354 | 6 | 3.1 | 172 | 5 | Q7VTR8 | Q7VTR8 caenorhabdi |
| 282 | 6 | 3.1 | 129 | 16 | Q8YTV1 | Q8YTV1 anabaena sp | 355 | 6 | 3.1 | 172 | 5 | Q7VTR8 | Q7VTR8 caenorhabdi |
| 283 | 6 | 3.1 | 130 | 16 | Q8Z0F0 | Q8Z0F0 anabaena sp | 356 | 6 | 3.1 | 172 | 11 | Q9R0C0 | Q9R0C0 mus musculus |
| 284 | 6 | 3.1 | 131 | 10 | Q94HR0 | Q94HR0 oryza sativ | 357 | 6 | 3.1 | 172 | 11 | Q9R0C0 | Q9R0C0 mus musculus |
| 285 | 6 | 3.1 | 131 | 10 | Q7XFU4 | Q7XFU4 oryza sativ | 358 | 6 | 3.1 | 173 | 8 | Q8HML1 | Q8HML1 lota lota (|
| 286 | 6 | 3.1 | 131 | 17 | Q9V0T3 | Q9V0T3 pyrococcus | 359 | 6 | 3.1 | 173 | 8 | Q8HML1 | Q8HML1 lota lota (|
| 287 | 6 | 3.1 | 131 | 17 | Q9V0T3 | Q9V0T3 pyrococcus | 360 | 6 | 3.1 | 173 | 8 | Q8HML1 | Q8HML1 lota lota (|
| 288 | 6 | 3.1 | 131 | 17 | Q9V0T3 | Q9V0T3 pyrococcus | 361 | 6 | 3.1 | 173 | 8 | Q8HML1 | Q8HML1 lota lota (|
| 289 | 6 | 3.1 | 132 | 10 | Q8SAA6 | Q8SAA6 arabidopsis | 362 | 6 | 3.1 | 174 | 16 | Q81GI2 | Q81GI2 bacillus ce |
| 290 | 6 | 3.1 | 132 | 10 | Q7XJVO | Q7XJVO oryza sativ | 363 | 6 | 3.1 | 174 | 16 | Q81GI2 | Q81GI2 bacillus ce |
| 291 | 6 | 3.1 | 132 | 16 | Q81KR6 | Q81KR6 bacillus an | 364 | 6 | 3.1 | 175 | 10 | Q9G605 | Q9G605 artibeus ja |
| 292 | 6 | 3.1 | 132 | 16 | Q81GZ0 | Q81GZ0 bacillus ce | 365 | 6 | 3.1 | 175 | 10 | Q9G605 | Q9G605 artibeus ja |
| 293 | 6 | 3.1 | 132 | 16 | Q7UR18 | Q7UR18 rhodopirell | 366 | 6 | 3.1 | 175 | 16 | Q8XUL8 | Q8XUL8 mus musculus |
| 294 | 6 | 3.1 | 132 | 16 | Q7UR18 | Q7UR18 rhodopirell | 367 | 6 | 3.1 | 176 | 2 | Q9EV88 | Q9EV88 mus musculus |
| 295 | 6 | 3.1 | 133 | 5 | Q9N1V7 | Q9N1V7 tegula brun | 368 | 6 | 3.1 | 176 | 2 | Q9EV88 | Q9EV88 mus musculus |
| 296 | 6 | 3.1 | 133 | 8 | Q36413 | Q36413 lachnaia sp | 369 | 6 | 3.1 | 176 | 2 | Q9EV88 | Q9EV88 mus musculus |
| 297 | 6 | 3.1 | 133 | 8 | Q36413 | Q36413 lachnaia sp | 370 | 6 | 3.1 | 177 | 5 | Q9VTC9 | Q9VTC9 drosophila |
| 298 | 6 | 3.1 | 133 | 8 | Q36413 | Q36413 lachnaia sp | 371 | 6 | 3.1 | 177 | 5 | Q9VTC9 | Q9VTC9 drosophila |
| 299 | 6 | 3.1 | 133 | 8 | Q36413 | Q36413 lachnaia sp | 372 | 6 | 3.1 | 177 | 5 | Q9VTC9 | Q9VTC9 drosophila |
| 300 | 6 | 3.1 | 135 | 17 | Q9E282 | Q9E282 sulfolobus | 373 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 301 | 6 | 3.1 | 135 | 17 | Q9E282 | Q9E282 sulfolobus | 374 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 302 | 6 | 3.1 | 136 | 16 | Q8DH91 | Q8DH91 yersinia pe | 375 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 303 | 6 | 3.1 | 136 | 16 | Q8DH91 | Q8DH91 yersinia pe | 376 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 304 | 6 | 3.1 | 136 | 16 | Q8DH91 | Q8DH91 yersinia pe | 377 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 305 | 6 | 3.1 | 138 | 16 | Q8ERQ6 | Q8ERQ6 oceanobacil | 378 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 306 | 6 | 3.1 | 140 | 8 | Q85FF8 | Q85FF8 cyanobacil | 379 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 307 | 6 | 3.1 | 141 | 11 | Q8BQ43 | Q8BQ43 mus musculus | 380 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| 308 | 6 | 3.1 | 142 | 11 | Q8C7N3 | Q8C7N3 mus musculus | 381 | 6 | 3.1 | 178 | 16 | Q8NNV5 | Q8NNV5 mus musculus |
| | 6 | 3.1 | 142 | 11 | Q8C7N3 | Q8C7N3 mus musculus | | | | | | | |
| | 6 | 3.1 | 143 | 16 | Q9ZKT3 | Q9ZKT3 helicobacte | | | | | | | |

| | | | | | | | | | | | |
|-----|---|-----|-----|----|--------|---------------------|-----|-----|----|--------|--------------------|
| 382 | 6 | 3.1 | 184 | 9 | Q9MC20 | Q9mc20 lactococcus | 455 | 206 | 16 | Q9RWY4 | Q9rwy4 deinococcus |
| 383 | 6 | 3.1 | 184 | 16 | Q9I0K2 | Q910k2 pseudomonas | 456 | 206 | 17 | Q8U0M1 | Q8u0m1 pyrococcus |
| 384 | 6 | 3.1 | 185 | 5 | Q22660 | Q22660 caenorhabdi | 457 | 206 | 17 | Q8THG9 | Q8thg9 methanosarc |
| 385 | 6 | 3.1 | 185 | 5 | Q86M77 | Q86m77 heterodera | 458 | 206 | 17 | Q8PXH6 | Q8pxh6 methanosarc |
| 386 | 6 | 3.1 | 185 | 10 | Q9MAI5 | Q9ma15 arabidopsis | 459 | 208 | 10 | Q9LGS1 | Q9lgs1 oryza sativ |
| 387 | 6 | 3.1 | 185 | 11 | Q8C4A9 | Q8c4a9 mus musculu | 460 | 208 | 10 | Q8S6A3 | Q8s6a3 oryza sativ |
| 388 | 6 | 3.1 | 185 | 11 | Q8BNX6 | Q8bnx6 mus musculu | 461 | 208 | 11 | Q9CVW7 | Q9cvw7 mus musculu |
| 389 | 6 | 3.1 | 185 | 17 | Q8PNW6 | Q8pnw6 methanosarc | 462 | 208 | 12 | Q8XJBO | Q8xjbo clostridium |
| 390 | 6 | 3.1 | 186 | 10 | Q9ZQH1 | Q9zqn1 arabidopsis | 463 | 208 | 16 | Q91FL9 | Q91fl9 chilo iride |
| 391 | 6 | 3.1 | 186 | 16 | Q9CNZ9 | Q9cnz9 pasteurella | 464 | 208 | 16 | Q8NZL6 | Q8nzi6 streptococc |
| 392 | 6 | 3.1 | 187 | 16 | Q8EBI8 | Q8ebi8 shewanella | 465 | 208 | 17 | Q970I9 | Q970i9 sulfobolus |
| 393 | 6 | 3.1 | 187 | 16 | Q7ZAN2 | Q7zan2 corynebacte | 466 | 209 | 10 | Q93488 | Q93488 colocasia e |
| 394 | 6 | 3.1 | 188 | 2 | Q52933 | Q52933 rhizobium m | 467 | 209 | 11 | Q9UKF4 | Q9ukf4 mus musculu |
| 395 | 6 | 3.1 | 188 | 6 | Q9GME4 | Q9gme4 callithrix | 468 | 210 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 396 | 6 | 3.1 | 188 | 16 | P74118 | P74118 synechocyst | 469 | 210 | 16 | Q9A6K8 | Q9a6k8 caulobacter |
| 397 | 6 | 3.1 | 189 | 5 | Q8IC97 | Q8ic97 plasmodium | 470 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 398 | 6 | 3.1 | 189 | 11 | Q7TMG5 | Q7tmg5 mus musculu | 471 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 399 | 6 | 3.1 | 190 | 4 | Q86WE3 | Q86we3 homo sapien | 472 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 400 | 6 | 3.1 | 190 | 11 | P70456 | P70456 mus musculu | 473 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 401 | 6 | 3.1 | 191 | 12 | Q99FP5 | Q99fp5 human echov | 474 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 402 | 6 | 3.1 | 191 | 4 | Q9HA76 | Q9ha76 homo sapien | 475 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 403 | 6 | 3.1 | 191 | 4 | Q9HAF1 | Q9haf1 homo sapien | 476 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 404 | 6 | 3.1 | 191 | 10 | Q8LFB3 | Q8lfb3 arabidopsis | 477 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 405 | 6 | 3.1 | 191 | 16 | Q8Y9P0 | Q8y9p0 listeria mo | 478 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 406 | 6 | 3.1 | 191 | 16 | Q8PCQ1 | Q8pcq1 xanthomonas | 479 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 407 | 6 | 3.1 | 191 | 16 | Q8LW93 | Q8lw93 macaca fasc | 480 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 408 | 6 | 3.1 | 192 | 11 | Q9D7J5 | Q9d7j5 mus musculu | 481 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 409 | 6 | 3.1 | 192 | 11 | Q9PW13 | Q9pw13 cynops ensi | 482 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 410 | 6 | 3.1 | 192 | 13 | Q8TY69 | Q8ty69 methanopyru | 483 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 411 | 6 | 3.1 | 193 | 6 | Q95KF9 | Q95kf9 macaca fasc | 484 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 412 | 6 | 3.1 | 193 | 16 | Q8RBB9 | Q8rbb9 thermomanaer | 485 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 413 | 6 | 3.1 | 194 | 16 | Q07001 | Q07001 bacillus su | 486 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 414 | 6 | 3.1 | 195 | 10 | Q8S2S7 | Q8s2s7 theillungiel | 487 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 415 | 6 | 3.1 | 195 | 17 | Q9TB70 | Q9tb70 thermoplas | 488 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 416 | 6 | 3.1 | 196 | 10 | Q9SWY4 | Q9swy4 dunaliella | 489 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 417 | 6 | 3.1 | 196 | 13 | P79827 | P79827 oncorhynch | 490 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 418 | 6 | 3.1 | 196 | 16 | Q8DGL7 | Q8dgl7 synecococc | 491 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 419 | 6 | 3.1 | 196 | 17 | Q9HRP6 | Q9hrp6 halobacteri | 492 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 420 | 6 | 3.1 | 197 | 2 | Q7X2R7 | Q7x2r7 rhizobium f | 493 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 421 | 6 | 3.1 | 197 | 5 | Q38872 | Q38872 dictyosteli | 494 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 422 | 6 | 3.1 | 197 | 16 | Q9JVD7 | Q9jvd7 neisseria m | 495 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 423 | 6 | 3.1 | 197 | 16 | Q8EDN3 | Q8edn3 shewanella | 496 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 424 | 6 | 3.1 | 197 | 16 | Q89TG1 | Q89tgi bradyrhizob | 497 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 425 | 6 | 3.1 | 198 | 2 | Q92B15 | Q92b15 leuconostoc | 498 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 426 | 6 | 3.1 | 198 | 16 | Q8REB6 | Q8rel6 fusobacteri | 499 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 427 | 6 | 3.1 | 199 | 10 | Q93386 | Q93386 brassica ol | 500 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 428 | 6 | 3.1 | 199 | 10 | Q84JX7 | Q84jx7 oryza sativ | 501 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 429 | 6 | 3.1 | 199 | 16 | Q8D3Q2 | Q8d3q2 vibrio vuln | 502 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 430 | 6 | 3.1 | 200 | 10 | Q9LWR5 | Q9lwr5 oryza sativ | 503 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 431 | 6 | 3.1 | 200 | 10 | Q8GVN7 | Q8gvn7 oryza sativ | 504 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 432 | 6 | 3.1 | 200 | 10 | Q9FZK5 | Q9fzk5 arabidopsis | 505 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 433 | 6 | 3.1 | 200 | 16 | Q8XE16 | Q8xel6 escherichia | 506 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 434 | 6 | 3.1 | 200 | 16 | Q8DDT4 | Q8ddt4 vibrio vuln | 507 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 435 | 6 | 3.1 | 200 | 16 | Q8CW04 | Q8cw04 escherichia | 508 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 436 | 6 | 3.1 | 200 | 16 | Q83BE2 | Q83be2 coxiella bu | 509 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 437 | 6 | 3.1 | 201 | 2 | Q9X7J0 | Q9x7j0 pseudomonas | 510 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 438 | 6 | 3.1 | 201 | 2 | Q9K4R3 | Q9k4r3 pseudomonas | 511 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 439 | 6 | 3.1 | 201 | 4 | Q7Z311 | Q7z311 homo sapien | 512 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 440 | 6 | 3.1 | 201 | 11 | Q9CVP8 | Q9cvp8 mus musculu | 513 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 441 | 6 | 3.1 | 201 | 11 | Q8BXD1 | Q8bxdl mus musculu | 514 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 442 | 6 | 3.1 | 202 | 16 | Q8YJ34 | Q8y34 pseudomonas | 515 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 443 | 6 | 3.1 | 203 | 16 | Q8S581 | Q8s581 synechocyst | 516 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 444 | 6 | 3.1 | 203 | 16 | Q83KR4 | Q83kr4 shigella fl | 517 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 445 | 6 | 3.1 | 203 | 16 | Q83AE8 | Q83ae8 shigella fl | 518 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 446 | 6 | 3.1 | 204 | 1 | Q49175 | Q49175 methanother | 519 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 447 | 6 | 3.1 | 204 | 16 | Q8E2Q5 | Q8e2q5 streptococc | 520 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 448 | 6 | 3.1 | 204 | 16 | Q99XK6 | Q99xk6 streptococc | 521 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 449 | 6 | 3.1 | 205 | 10 | Q7XZ29 | Q7xz29 griffithsia | 522 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 450 | 6 | 3.1 | 205 | 11 | Q8BMX2 | Q8bm2 mus musculu | 523 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 451 | 6 | 3.1 | 205 | 12 | Q9QPF8 | Q9qpf8 hepatitis e | 524 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 452 | 6 | 3.1 | 205 | 16 | Q97RX0 | Q97rx0 streptococc | 525 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 453 | 6 | 3.1 | 205 | 16 | Q88NJ1 | Q88nj1 pseudomonas | 526 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |
| 454 | 6 | 3.1 | 206 | 3 | Q9P533 | Q9p533 neurospora | 527 | 211 | 2 | Q9K2G9 | Q9k2g9 streptococc |

| | | | | | | | | | | | | | |
|-----|---|-----|-----|----|--------|---------------------|-----|---|-----|-----|----|--------|---------------------|
| 528 | 6 | 3.1 | 226 | 16 | Q8FTF5 | Q8ftf5 corynebacte | 601 | 6 | 3.1 | 252 | 5 | Q9N4C7 | Q9n4c7 caenorhabdi |
| 529 | 6 | 3.1 | 226 | 17 | O59384 | O59384 pyrococcus | 602 | 6 | 3.1 | 252 | 10 | Q9SP21 | Q9sp21 boea crassi |
| 530 | 6 | 3.1 | 227 | 16 | Q8P8V9 | Q8p8v9 xanthomonas | 603 | 6 | 3.1 | 252 | 16 | Q8FNM6 | Q8fnm6 corynebacte |
| 531 | 6 | 3.1 | 227 | 16 | Q9L2G6 | Q9l2g6 streptomyc | 604 | 6 | 3.1 | 252 | 16 | Q88YH4 | Q88yh4 lactobacill |
| 532 | 6 | 3.1 | 227 | 16 | Q82B09 | Q82b09 streptomyc | 605 | 6 | 3.1 | 252 | 16 | Q81A80 | Q81a80 bacillus ce |
| 533 | 6 | 3.1 | 228 | 10 | Q9LMK7 | Q9lmk7 arabadopsi | 606 | 6 | 3.1 | 252 | 17 | Q97A60 | Q97a60 thermoplas |
| 534 | 6 | 3.1 | 229 | 5 | Q94195 | Q94195 caenorhabdi | 607 | 6 | 3.1 | 253 | 2 | Q9X4R1 | Q9x4r1 enterococu |
| 535 | 6 | 3.1 | 230 | 16 | Q88NT3 | Q88nt3 pseudomonas | 608 | 6 | 3.1 | 253 | 10 | Q22082 | Q22082 patunia hyb |
| 536 | 6 | 3.1 | 231 | 16 | Q7WK40 | Q7wk40 bordetella | 609 | 6 | 3.1 | 253 | 13 | Q9DDF5 | Q9ddf5 gallus gall |
| 537 | 6 | 3.1 | 231 | 16 | Q7W8T0 | Q7w8t0 bordetella | 610 | 6 | 3.1 | 254 | 16 | Q97S14 | Q97s14 streptococc |
| 538 | 6 | 3.1 | 231 | 16 | Q7VZ31 | Q7vz31 pyrococcus | 611 | 6 | 3.1 | 254 | 16 | Q67535 | Q67535 aquifex aeo |
| 539 | 6 | 3.1 | 231 | 17 | Q8UOV8 | Q8uov8 pyrococcus | 612 | 6 | 3.1 | 256 | 11 | Q7XKH2 | Q7xkh2 oryza sativ |
| 540 | 6 | 3.1 | 232 | 10 | Q9ST20 | Q9st20 brassica ca | 613 | 6 | 3.1 | 256 | 13 | Q42139 | Q42139 xenopus lae |
| 541 | 6 | 3.1 | 232 | 16 | Q8G5N9 | Q8g5n9 bifidobacte | 614 | 6 | 3.1 | 257 | 12 | Q98ZP5 | Q98zp5 potato viru |
| 542 | 6 | 3.1 | 232 | 17 | Q9VLL2 | Q9vll2 pyrococcus | 615 | 6 | 3.1 | 257 | 16 | Q8F6V2 | Q8f6v2 leptospira |
| 543 | 6 | 3.1 | 233 | 12 | Q91TV2 | Q91tv2 tupaia herp | 616 | 6 | 3.1 | 257 | 16 | Q8F6V2 | Q8f6v2 leptospira |
| 544 | 6 | 3.1 | 233 | 10 | Q949V7 | Q949v7 arabadopsi | 617 | 6 | 3.1 | 258 | 5 | Q19326 | Q19326 caenorhabdi |
| 545 | 6 | 3.1 | 234 | 10 | Q04149 | Q04149 arabadopsi | 618 | 6 | 3.1 | 258 | 10 | Q9XIC2 | Q9xic2 arabadopsi |
| 546 | 6 | 3.1 | 234 | 10 | Q9XHS1 | Q9xhs1 arabadopsi | 619 | 6 | 3.1 | 258 | 12 | Q81861 | Q81861 heparitis e |
| 547 | 6 | 3.1 | 234 | 16 | Q8K8Q7 | Q8k8q7 streptococc | 620 | 6 | 3.1 | 258 | 16 | Q9K4B7 | Q9k4b7 streptomyc |
| 548 | 6 | 3.1 | 236 | 16 | Q8RVH6 | Q8rvh6 deinococcc | 621 | 6 | 3.1 | 258 | 16 | Q8EPP5 | Q8ep5 oceanobacil |
| 549 | 6 | 3.1 | 236 | 16 | Q8F9V4 | Q8f9v4 leptospira | 622 | 6 | 3.1 | 259 | 10 | Q7XS97 | Q7xs97 oryza sativ |
| 550 | 6 | 3.1 | 236 | 16 | Q7U4E2 | Q7u4e2 synecococc | 623 | 6 | 3.1 | 260 | 11 | Q8CEW5 | Q8cew5 mus musculu |
| 551 | 6 | 3.1 | 237 | 7 | Q31466 | Q31466 morone saxa | 624 | 6 | 3.1 | 260 | 11 | Q8BMX8 | Q8bm8 mus musculu |
| 552 | 6 | 3.1 | 237 | 10 | Q9LUC7 | Q9luc7 arabadopsi | 625 | 6 | 3.1 | 260 | 16 | Q9KRC5 | Q9kr5 vibrio chol |
| 553 | 6 | 3.1 | 238 | 5 | Q8STH9 | Q8st9 encephalito | 626 | 6 | 3.1 | 260 | 16 | Q9HYV6 | Q9hyv6 pseudomonas |
| 554 | 6 | 3.1 | 238 | 16 | Q7W9Q9 | Q7w9z9 bordetella | 627 | 6 | 3.1 | 262 | 10 | Q9M3C1 | Q9m3c1 arabadopsi |
| 555 | 6 | 3.1 | 238 | 16 | Q7W9B7 | Q7w9g9 bordetella | 628 | 6 | 3.1 | 262 | 16 | Q8X8R8 | Q8x8r8 escherichia |
| 556 | 6 | 3.1 | 238 | 17 | Q8TJK7 | Q8tjk7 bordetella | 629 | 6 | 3.1 | 262 | 16 | Q7UVY7 | Q7uvy7 rhodopirell |
| 557 | 6 | 3.1 | 238 | 17 | Q8TJK7 | Q8tjk7 methanosarc | 630 | 6 | 3.1 | 262 | 2 | Q7X3Q9 | Q7x3q9 staphylococ |
| 558 | 6 | 3.1 | 239 | 5 | Q9VIU0 | Q9viu0 drosophila | 631 | 6 | 3.1 | 263 | 5 | Q9GUD6 | Q9gud6 habesia big |
| 559 | 6 | 3.1 | 239 | 10 | Q8LA42 | Q8la42 arabadopsi | 632 | 6 | 3.1 | 263 | 5 | Q9GNT5 | Q9gni5 babesia big |
| 560 | 6 | 3.1 | 239 | 10 | Q8H5V6 | Q8h5v6 oryza sativ | 633 | 6 | 3.1 | 263 | 13 | Q803P1 | Q803p1 brachydanio |
| 561 | 6 | 3.1 | 239 | 16 | Q89S50 | Q89s50 clostridium | 634 | 6 | 3.1 | 263 | 16 | Q87QW5 | Q87qw5 vibrio para |
| 562 | 6 | 3.1 | 239 | 16 | Q82BT0 | Q82bt0 streptomyc | 635 | 6 | 3.1 | 264 | 11 | Q8BWM4 | Q8bwm4 mus musculu |
| 563 | 6 | 3.1 | 240 | 4 | Q8TED2 | Q8ted2 homo sapien | 636 | 6 | 3.1 | 264 | 16 | Q9RUN3 | Q9run3 deinococcus |
| 564 | 6 | 3.1 | 240 | 16 | Q8R9H7 | Q8r9h7 thermococcc | 637 | 6 | 3.1 | 264 | 16 | Q8CWT1 | Q8cwt1 streptococc |
| 565 | 6 | 3.1 | 240 | 16 | Q8P2R5 | Q8p2r5 streptococc | 638 | 6 | 3.1 | 265 | 2 | Q9AMZ4 | Q9amz4 bradyrhizob |
| 566 | 6 | 3.1 | 241 | 4 | Q9NPF4 | Q9np64 homo sapien | 639 | 6 | 3.1 | 265 | 5 | P90819 | P90819 caenorhabdi |
| 567 | 6 | 3.1 | 241 | 11 | Q9ESX4 | Q9esx4 mus musculu | 640 | 6 | 3.1 | 265 | 5 | P90819 | P90819 streptococc |
| 568 | 6 | 3.1 | 241 | 11 | Q9ESX4 | Q9esx4 mus musculu | 641 | 6 | 3.1 | 266 | 2 | Q93MY2 | Q93my2 streptococc |
| 569 | 6 | 3.1 | 242 | 13 | Q9YH13 | Q9yh13 gallus gall | 642 | 6 | 3.1 | 266 | 3 | Q42898 | Q42898 schizosacch |
| 570 | 6 | 3.1 | 242 | 13 | Q7ZV17 | Q7zv17 brachydanio | 643 | 6 | 3.1 | 266 | 3 | Q42898 | Q42898 schizosacch |
| 571 | 6 | 3.1 | 242 | 17 | Q9HLV4 | Q9hlv4 thermoplas | 644 | 6 | 3.1 | 267 | 5 | Q86DV4 | Q86dv4 schistosoma |
| 572 | 6 | 3.1 | 242 | 11 | Q9CTE2 | Q9ctt2 mus musculu | 645 | 6 | 3.1 | 267 | 5 | Q86DV4 | Q86dv4 schistosoma |
| 573 | 6 | 3.1 | 243 | 16 | Q69830 | Q69830 streptomyc | 646 | 6 | 3.1 | 267 | 5 | Q9BDK9 | Q9bdk9 sus scrofa |
| 574 | 6 | 3.1 | 244 | 16 | Q7U4R3 | Q7u4r3 synecococc | 647 | 6 | 3.1 | 267 | 10 | Q9MSU2 | Q9msu2 arabadopsi |
| 575 | 6 | 3.1 | 245 | 2 | Q31394 | Q31394 bacillus me | 648 | 6 | 3.1 | 267 | 12 | Q9LH75 | Q9lh75 cherry necr |
| 576 | 6 | 3.1 | 245 | 16 | Q9KUE6 | Q9kue6 vibrio chol | 649 | 6 | 3.1 | 267 | 13 | Q9PUV0 | Q9puv0 balistes sp |
| 577 | 6 | 3.1 | 245 | 16 | Q8KEM0 | Q8kemo chlorobium | 650 | 6 | 3.1 | 267 | 16 | Q8DT65 | Q8dt65 streptococc |
| 578 | 6 | 3.1 | 245 | 16 | Q8F4X1 | Q8f4x1 leptospira | 651 | 6 | 3.1 | 268 | 9 | Q8SDW2 | Q8sdw2 bacterioph |
| 579 | 6 | 3.1 | 245 | 16 | Q8F4X1 | Q8f4x1 leptospira | 652 | 6 | 3.1 | 268 | 9 | Q8SDW2 | Q8sdw2 bacterioph |
| 580 | 6 | 3.1 | 246 | 2 | Q81043 | Q81043 azospirillum | 653 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 581 | 6 | 3.1 | 246 | 2 | Q9F7F1 | Q9f7f1 azospirillum | 654 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 582 | 6 | 3.1 | 246 | 5 | Q9BHA3 | Q9bha3 sabelia spa | 655 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 583 | 6 | 3.1 | 247 | 10 | Q84TE5 | Q84te5 arabadopsi | 656 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 584 | 6 | 3.1 | 247 | 16 | Q7WH87 | Q7wh87 bordetella | 657 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 585 | 6 | 3.1 | 247 | 16 | Q7WH87 | Q7wh87 bordetella | 658 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 586 | 6 | 3.1 | 248 | 5 | Q81S06 | Q81s06 bugia mala | 659 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 587 | 6 | 3.1 | 248 | 12 | Q81860 | Q81860 heparitis e | 660 | 6 | 3.1 | 269 | 2 | Q8KLS6 | Q8kl56 rhodobacter |
| 588 | 6 | 3.1 | 248 | 17 | Q9PUW2 | Q9puw2 methanosarc | 661 | 6 | 3.1 | 269 | 10 | Q39647 | Q39647 cucurbita c |
| 589 | 6 | 3.1 | 249 | 10 | Q7X9H6 | Q7x9h6 arabadopsi | 662 | 6 | 3.1 | 269 | 16 | Q9RCS5 | Q9rcs5 streptococc |
| 590 | 6 | 3.1 | 249 | 13 | Q7SXU0 | Q7sxu0 brachydanio | 663 | 6 | 3.1 | 269 | 16 | Q8RBS9 | Q8res9 fusobacteri |
| 591 | 6 | 3.1 | 249 | 16 | Q97HF0 | Q97hf0 clostridium | 664 | 6 | 3.1 | 269 | 16 | Q8EXV5 | Q8exv5 leptospira |
| 592 | 6 | 3.1 | 249 | 16 | Q97HF0 | Q97hf0 clostridium | 665 | 6 | 3.1 | 269 | 16 | Q8DPL9 | Q8dpl9 streptococc |
| 593 | 6 | 3.1 | 249 | 16 | Q25574 | Q25574 helicobacte | 666 | 6 | 3.1 | 269 | 16 | Q8DAQ1 | Q8daq1 vibrio vuln |
| 594 | 6 | 3.1 | 249 | 16 | Q8G2E1 | Q8g2e1 bruceella su | 667 | 6 | 3.1 | 269 | 16 | Q8DAQ1 | Q8daq1 vibrio vuln |
| 595 | 6 | 3.1 | 250 | 5 | P90779 | P90779 caenorhabdi | 668 | 6 | 3.1 | 269 | 16 | Q9A106 | Q9a106 streptococc |
| 596 | 6 | 3.1 | 250 | 10 | Q9LMV5 | Q9lmv5 arabadopsi | 669 | 6 | 3.1 | 270 | 2 | Q9RCK9 | Q9rcck9 streptococc |
| 597 | 6 | 3.1 | 250 | 16 | Q8EPK7 | Q8epk7 oceanobacil | 670 | 6 | 3.1 | 270 | 2 | Q9RCK9 | Q9rcck9 streptococc |
| 598 | 6 | 3.1 | 250 | 16 | Q8ZNE4 | Q8zne4 streptomyc | 671 | 6 | 3.1 | 270 | 2 | Q9RCK9 | Q9rcck9 streptococc |
| 599 | 6 | 3.1 | 251 | 2 | Q9RQW8 | Q9rqw8 neisseria m | 672 | 6 | 3.1 | 270 | 2 | Q9RCK9 | Q9rcck9 streptococc |
| 600 | 6 | 3.1 | 251 | 2 | Q9RMN8 | Q9rmn8 neisseria m | 673 | 6 | 3.1 | 270 | 2 | Q9RCK9 | Q9rcck9 streptococc |
| | | | | | | Q9li72 arabadopsi | | | | | | | |

| | | | | | | | | | | | | |
|-----|---|-----|-----|----|---------|---------------------|-----|-----|-----|----|--------|--------------------|
| 674 | 6 | 3.1 | 281 | 16 | Q9CKM7 | Q9ckm7 pasteurella | 747 | 3.1 | 302 | 10 | Q22066 | Q22066 arabidopsis |
| 675 | 6 | 3.1 | 282 | 2 | Q9R6G8 | Q9r6g8 agrobacteri | 748 | 3.1 | 302 | 10 | Q8LP01 | Q8lp01 arabis gemm |
| 676 | 6 | 3.1 | 282 | 5 | Q9GUD5 | Q9gud5 babesia big | 749 | 3.1 | 302 | 10 | Q22072 | Q22072 arabidopsis |
| 677 | 6 | 3.1 | 282 | 5 | Q9GUD2 | Q9gud2 babesia big | 750 | 3.1 | 302 | 10 | Q22068 | Q22068 arabidopsis |
| 678 | 6 | 3.1 | 282 | 5 | Q9GUD4 | Q9gud4 babesia big | 751 | 3.1 | 302 | 10 | Q22065 | Q22065 arabidopsis |
| 679 | 6 | 3.1 | 282 | 5 | Q9GUD3 | Q9gud3 babesia big | 752 | 3.1 | 302 | 10 | Q8LP04 | Q8lp04 arabis gemm |
| 680 | 6 | 3.1 | 282 | 5 | O15708 | O15708 babesia big | 753 | 3.1 | 302 | 10 | Q8LP04 | Q8lp04 arabis gemm |
| 681 | 6 | 3.1 | 282 | 2 | Q05342 | Q05342 versinia ps | 754 | 3.1 | 302 | 10 | Q22074 | Q22074 arabis gemm |
| 682 | 6 | 3.1 | 283 | 2 | Q05342 | Q05342 versinia ps | 755 | 3.1 | 302 | 10 | Q22074 | Q22074 arabis gemm |
| 683 | 6 | 3.1 | 283 | 10 | Q81802 | Q81802 arabidopsis | 756 | 3.1 | 302 | 10 | Q8LP02 | Q8lp02 arabis gemm |
| 684 | 6 | 3.1 | 283 | 16 | Q988E7 | Q988e7 rhizobium l | 757 | 3.1 | 302 | 10 | Q8LP06 | Q8lp06 arabis glab |
| 685 | 6 | 3.1 | 283 | 16 | Q9RJF9 | Q9rjf9 streptomyce | 758 | 3.1 | 302 | 10 | Q22075 | Q22075 arabidopsis |
| 686 | 6 | 3.1 | 284 | 10 | Q40595 | Q40595 nicotiana t | 759 | 3.1 | 302 | 10 | Q22069 | Q22069 arabidopsis |
| 687 | 6 | 3.1 | 285 | 16 | Q97DX1 | Q97dx1 clostridium | 760 | 3.1 | 302 | 10 | Q22067 | Q22067 arabidopsis |
| 688 | 6 | 3.1 | 285 | 16 | Q2L0X4 | Q2l0x4 streptomyce | 761 | 3.1 | 302 | 16 | Q7WF30 | Q7wf30 bordetella |
| 689 | 6 | 3.1 | 285 | 16 | Q8DVP2 | Q8dvp2 streptococc | 762 | 3.1 | 302 | 16 | Q7W3Q3 | Q7w3q3 bordetella |
| 690 | 6 | 3.1 | 286 | 5 | Q9GQS1 | Q9gqs1 meloidogyne | 763 | 3.1 | 302 | 16 | Q7VST9 | Q7vst9 bordetella |
| 691 | 6 | 3.1 | 286 | 10 | Q8W507 | Q8w507 nicotiana t | 764 | 3.1 | 302 | 16 | Q7U653 | Q7u653 synecococc |
| 692 | 6 | 3.1 | 286 | 10 | O81013 | O81013 arabidopsis | 765 | 3.1 | 303 | 10 | Q64761 | Q64761 arabidopsis |
| 693 | 6 | 3.1 | 286 | 10 | O81YV1 | O81yv1 arabidopsis | 766 | 3.1 | 303 | 16 | Q55483 | Q55483 synecocyst |
| 694 | 6 | 3.1 | 286 | 16 | Q9ZL77 | Q9zl77 helicobacte | 767 | 3.1 | 303 | 16 | Q8NTU5 | Q8ntus corynebacte |
| 695 | 6 | 3.1 | 287 | 10 | Q8LEK3 | Q8lek3 arabidopsis | 768 | 3.1 | 305 | 16 | Q82LI5 | Q82li5 streptomyce |
| 696 | 6 | 3.1 | 287 | 10 | O92224 | O92224 nicotiana e | 769 | 3.1 | 306 | 5 | Q7Z0G8 | Q7z0g8 metapeneus |
| 697 | 6 | 3.1 | 287 | 10 | Q9LTV3 | Q9ltv3 arabidopsis | 770 | 3.1 | 306 | 11 | Q8C742 | Q8c742 mus musculu |
| 698 | 6 | 3.1 | 288 | 2 | Q9AKE5 | Q9ake5 rickettsia | 771 | 3.1 | 306 | 16 | Q8XA42 | Q8xa42 escherichia |
| 699 | 6 | 3.1 | 288 | 8 | Q35993 | Q35993 trypanosoma | 772 | 3.1 | 306 | 16 | Q8XVC8 | Q8xvc8 ralstonia s |
| 700 | 6 | 3.1 | 288 | 10 | Q9XGF4 | Q9xgf4 solanum tub | 773 | 3.1 | 306 | 16 | Q8FF21 | Q8ff21 escherichia |
| 701 | 6 | 3.1 | 288 | 10 | O23771 | O23771 cratereostig | 774 | 3.1 | 306 | 16 | Q83K34 | Q83k34 shigella fl |
| 702 | 6 | 3.1 | 289 | 10 | O23272 | O23272 arabidopsis | 775 | 3.1 | 307 | 10 | Q94JVS | Q94jvs arabidopsis |
| 703 | 6 | 3.1 | 289 | 10 | Q38911 | Q38911 arabidopsis | 776 | 3.1 | 307 | 16 | Q89HT1 | Q89ht1 bradyrhizob |
| 704 | 6 | 3.1 | 289 | 12 | Q9YILL1 | Q9yll1 human echov | 777 | 3.1 | 308 | 2 | Q93E11 | Q93e11 rhizobium l |
| 705 | 6 | 3.1 | 289 | 16 | O81X64 | O81x64 bacillus an | 778 | 3.1 | 309 | 5 | Q9VED5 | Q9ved5 drosophila |
| 706 | 6 | 3.1 | 289 | 17 | Q96ZX0 | Q96zx0 sulfolobus | 779 | 3.1 | 309 | 5 | Q81GM9 | Q81gm9 drosophila |
| 707 | 6 | 3.1 | 290 | 2 | Q9AQX4 | Q9akx4 rickettsia | 780 | 3.1 | 310 | 16 | Q82VX5 | Q82vx5 nitrosomona |
| 708 | 6 | 3.1 | 290 | 2 | Q9AKX0 | Q9akx0 rickettsia | 781 | 3.1 | 310 | 16 | Q8ENQ7 | Q8enq7 oceanobacil |
| 709 | 6 | 3.1 | 290 | 12 | Q8B912 | Q8b912 racchiplusia | 782 | 3.1 | 312 | 2 | Q59456 | Q59456 halobacteri |
| 710 | 6 | 3.1 | 291 | 10 | Q8LG58 | Q8lg58 arabidopsis | 783 | 3.1 | 312 | 2 | P72457 | P72457 streptomyce |
| 711 | 6 | 3.1 | 291 | 10 | Q9LK45 | Q9lk45 arabidopsis | 784 | 3.1 | 312 | 16 | O26068 | O26068 helicobacte |
| 712 | 6 | 3.1 | 291 | 10 | Q7XZP8 | Q7xzp8 oryza sativ | 785 | 3.1 | 312 | 16 | O67040 | O67040 aquifex aso |
| 713 | 6 | 3.1 | 291 | 17 | Q8TVS0 | Q8tyv0 methanopyru | 786 | 3.1 | 312 | 16 | Q9ZJ59 | Q9zj59 helicobacte |
| 714 | 6 | 3.1 | 292 | 10 | Q8GRL4 | Q8grl4 oryza sativ | 787 | 3.1 | 312 | 16 | Q7U4U4 | Q7uau4 shigella fl |
| 715 | 6 | 3.1 | 292 | 11 | Q7TQ94 | Q7tq94 rattus norv | 788 | 3.1 | 312 | 17 | Q9HOK0 | Q9hqk0 halobacteri |
| 716 | 6 | 3.1 | 293 | 10 | O49876 | O49876 lupinus alb | 789 | 3.1 | 313 | 4 | Q9UKA0 | Q9uka0 homo sapien |
| 717 | 6 | 3.1 | 294 | 5 | Q9W0A9 | Q9w0a9 drosophila | 790 | 3.1 | 314 | 16 | Q82FY5 | Q82fy5 streptomyce |
| 718 | 6 | 3.1 | 294 | 16 | Q7W5M2 | Q7w5m2 bordetella | 791 | 3.1 | 315 | 5 | Q20123 | Q20123 caenorhabdi |
| 719 | 6 | 3.1 | 294 | 16 | Q7VW63 | Q7vw63 bordetella | 792 | 3.1 | 315 | 16 | Q8ZGD8 | Q8zgd8 yerinia pe |
| 720 | 6 | 3.1 | 295 | 2 | O66147 | O66147 plectonema | 793 | 3.1 | 316 | 10 | Q9LE50 | Q9le50 arabidopsis |
| 721 | 6 | 3.1 | 295 | 10 | Q8LP08 | Q8lp08 crucihmala | 794 | 3.1 | 316 | 16 | Q9HXK2 | Q9hxx2 pseudomonas |
| 722 | 6 | 3.1 | 295 | 10 | Q8LP05 | Q8lp05 crucihmala | 795 | 3.1 | 316 | 16 | Q8RC66 | Q8rc66 thermomona |
| 723 | 6 | 3.1 | 295 | 10 | Q8LP07 | Q8lp07 olimarabido | 796 | 3.1 | 316 | 16 | Q8RC66 | Q8rc66 thermomona |
| 724 | 6 | 3.1 | 296 | 16 | Q8XEM0 | Q8xem0 ralstonia s | 797 | 3.1 | 317 | 16 | Q8RC66 | Q8rc66 thermomona |
| 725 | 6 | 3.1 | 297 | 16 | Q8UA53 | Q8ua53 agrobacteri | 798 | 3.1 | 318 | 16 | Q9JUN5 | Q9jns5 neisseria m |
| 726 | 6 | 3.1 | 298 | 4 | O75628 | O75628 homo sapien | 799 | 3.1 | 318 | 16 | Q8F9Q7 | Q8f9q7 leptospira |
| 727 | 6 | 3.1 | 298 | 4 | Q9NP57 | Q9np57 homo sapien | 800 | 3.1 | 319 | 16 | Q92PG1 | Q92pg1 rhizobium m |
| 728 | 6 | 3.1 | 298 | 10 | Q9SXM5 | Q9sxm5 glycine max | 801 | 3.1 | 320 | 4 | Q8N4Q3 | Q8n4q3 homo sapien |
| 729 | 6 | 3.1 | 298 | 10 | Q9XGB4 | Q9xgb4 trifolium r | 802 | 3.1 | 320 | 17 | Q8ZT08 | Q8zt08 pyrobaculum |
| 730 | 6 | 3.1 | 298 | 16 | Q8PDI3 | Q8pdi3 xanthomonas | 803 | 3.1 | 321 | 2 | Q9XCT6 | Q9xc6 pseudomonas |
| 731 | 6 | 3.1 | 298 | 16 | Q886U8 | Q886u8 pseudomonas | 804 | 3.1 | 321 | 2 | Q9XCZ3 | Q9xc3 pseudomonas |
| 732 | 6 | 3.1 | 299 | 10 | Q9S7G9 | Q9s7g9 glycine max | 805 | 3.1 | 321 | 5 | Q867V1 | Q867v1 drosophila |
| 733 | 6 | 3.1 | 299 | 10 | P81258 | P81258 brassica na | 806 | 3.1 | 321 | 16 | Q83CU5 | Q83cu5 coxiella bu |
| 734 | 6 | 3.1 | 300 | 11 | Q8BY15 | Q8by15 mus musculu | 807 | 3.1 | 321 | 16 | Q83CU5 | Q83cu5 coxiella bu |
| 735 | 6 | 3.1 | 300 | 11 | Q8BY15 | Q8by15 mus musculu | 808 | 3.1 | 322 | 5 | Q86C07 | Q86c07 drosophila |
| 736 | 6 | 3.1 | 300 | 16 | Q9RUY6 | Q9ruy6 deinoococc | 809 | 3.1 | 322 | 5 | Q86C06 | Q86c06 drosophila |
| 737 | 6 | 3.1 | 301 | 11 | Q8BN70 | Q8bn70 mus musculu | 810 | 3.1 | 322 | 5 | Q86C05 | Q86c05 drosophila |
| 738 | 6 | 3.1 | 301 | 16 | Q87J47 | Q87j47 vibrio para | 811 | 3.1 | 322 | 5 | Q867Y1 | Q867y1 drosophila |
| 739 | 6 | 3.1 | 301 | 16 | Q83B50 | Q83b50 coxiella bu | 812 | 3.1 | 322 | 5 | Q7Z0G9 | Q7z0g9 metapeneus |
| 740 | 6 | 3.1 | 302 | 10 | Q22076 | Q22076 arabidopsis | 813 | 3.1 | 322 | 10 | Q9AR42 | Q9ar42 oryza sativ |
| 741 | 6 | 3.1 | 302 | 10 | Q22070 | Q22070 arabidopsis | 814 | 3.1 | 322 | 12 | Q9Q6P9 | Q9qp9 grapevine l |
| 742 | 6 | 3.1 | 302 | 10 | Q8LP09 | Q8lp09 arabidopsis | 815 | 3.1 | 322 | 16 | Q926E8 | Q926e8 rhizobium m |
| 743 | 6 | 3.1 | 302 | 10 | O22073 | O22073 arabidopsis | 816 | 3.1 | 322 | 16 | Q8PDR4 | Q8pdr4 xanthomonas |
| 744 | 6 | 3.1 | 302 | 10 | Q8LP03 | Q8lp03 arabis gemm | 817 | 3.1 | 323 | 2 | Q9XCZ5 | Q9xcz5 pseudomonas |
| 745 | 6 | 3.1 | 302 | 10 | Q8L4Q9 | Q8l4q9 arabis gemm | 818 | 3.1 | 323 | 4 | Q8N4M3 | Q8n4m3 homo sapien |
| 746 | 6 | 3.1 | 302 | 10 | O22071 | O22071 arabidopsis | 819 | 3.1 | 323 | 4 | Q8N4M3 | Q8n4m3 homo sapien |

| | | | | | | | | | | | |
|-----|-----|-----|----|---------|---------------------|-----|---|-----|----|--------|---------------------|
| 820 | 3.1 | 323 | 11 | Q9RLN4 | Q9RLN4 mus musculus | 893 | 6 | 3.1 | 4 | Q9NZK9 | Q9NZK9 homo sapien |
| 821 | 3.1 | 323 | 11 | Q8526 | Q8526 mus musculus | 894 | 6 | 3.1 | 11 | Q8CHS4 | Q8CHS4 mus musculus |
| 822 | 3.1 | 323 | 11 | Q8VDK1 | Q8VDK1 mus musculus | 895 | 6 | 3.1 | 16 | Q7V0H0 | Q7V0H0 prochloroco |
| 823 | 3.1 | 323 | 16 | Q8PQNS | Q8PQNS xanthomonas | 896 | 6 | 3.1 | 5 | Q9U0G0 | Q9U0G0 plasmodium |
| 824 | 3.1 | 324 | 2 | Q8KIK7 | Q8KIK7 rhizobium e | 897 | 6 | 3.1 | 10 | Q8LLN2 | Q8LLN2 oryza sativ |
| 825 | 3.1 | 324 | 13 | Q10727 | Q10727 gallus gall | 898 | 6 | 3.1 | 16 | Q9XIR1 | Q9XIR1 thermotoga |
| 826 | 3.1 | 324 | 17 | Q8PT59 | Q8PT59 methanosarc | 899 | 6 | 3.1 | 16 | Q9KF84 | Q9KF84 bacillus ha |
| 827 | 3.1 | 324 | 17 | Q8PW59 | Q8PW59 methanosarc | 900 | 6 | 3.1 | 16 | Q9JVR8 | Q9JVR8 neisseria m |
| 828 | 3.1 | 325 | 5 | Q44016 | Q44016 dictyosteli | 901 | 6 | 3.1 | 16 | Q8FFZ0 | Q8FFZ0 escherichia |
| 829 | 3.1 | 325 | 10 | Q9A4J6 | Q9A4J6 arabidopsis | 902 | 6 | 3.1 | 16 | Q88DC3 | Q88DC3 pseudomonas |
| 830 | 3.1 | 325 | 16 | Q9A453 | Q9A453 caulobacter | 903 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 831 | 3.1 | 326 | 4 | Q8NBR4 | Q8NBR4 homo sapien | 904 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 832 | 3.1 | 326 | 10 | Q9FTJ6 | Q9FTJ6 oryza sativ | 905 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 833 | 3.1 | 326 | 16 | Q8YF22 | Q8YF22 anabaena sp | 906 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 834 | 3.1 | 327 | 10 | Q8LKP1 | Q8LKP1 hordeum spo | 907 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 835 | 3.1 | 327 | 10 | Q8LKP2 | Q8LKP2 hordeum vul | 908 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 836 | 3.1 | 327 | 10 | Q8LKP3 | Q8LKP3 hordeum vul | 909 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 837 | 3.1 | 328 | 2 | Q9XCZ7 | Q9XCZ7 pseudomonas | 910 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 838 | 3.1 | 328 | 5 | Q9NFV9 | Q9NFV9 plasmodium | 911 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 839 | 3.1 | 329 | 10 | Q8H285 | Q8H285 ananas como | 912 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 840 | 3.1 | 330 | 16 | Q8FW40 | Q8FW40 brucella su | 913 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 841 | 3.1 | 330 | 16 | Q88AE5 | Q88AE5 pseudomonas | 914 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 842 | 3.1 | 331 | 10 | Q82282 | Q82282 arabidopsis | 915 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 843 | 3.1 | 331 | 16 | Q8X6V8 | Q8X6V8 escherichia | 916 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 844 | 3.1 | 331 | 16 | Q83PV1 | Q83PV1 shigella fl | 917 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 845 | 3.1 | 332 | 2 | Q841U3 | Q841U3 vibrio vuln | 918 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 846 | 3.1 | 333 | 4 | Q9NUR4 | Q9NUR4 homo sapien | 919 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 847 | 3.1 | 333 | 5 | Q95VQ2 | Q95VQ2 franklini | 920 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 848 | 3.1 | 333 | 5 | Q95VQ4 | Q95VQ4 franklini | 921 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 849 | 3.1 | 333 | 16 | Q8DBN6 | Q8DBN6 vibrio vuln | 922 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 850 | 3.1 | 334 | 5 | Q95VQ3 | Q95VQ3 streptomyce | 923 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 851 | 3.1 | 334 | 5 | Q95VQ1 | Q95VQ1 franklini | 924 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 852 | 3.1 | 334 | 5 | Q95VQ2 | Q95VQ2 franklini | 925 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 853 | 3.1 | 334 | 5 | Q95VQ1 | Q95VQ1 franklini | 926 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 854 | 3.1 | 334 | 5 | Q95VQ2 | Q95VQ2 franklini | 927 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 855 | 3.1 | 334 | 5 | Q95VQ3 | Q95VQ3 franklini | 928 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 856 | 3.1 | 334 | 5 | Q95VQ4 | Q95VQ4 franklini | 929 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 857 | 3.1 | 334 | 5 | Q95VQ5 | Q95VQ5 franklini | 930 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 858 | 3.1 | 334 | 5 | Q95VQ6 | Q95VQ6 franklini | 931 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 859 | 3.1 | 334 | 5 | Q95VQ7 | Q95VQ7 franklini | 932 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 860 | 3.1 | 334 | 5 | Q95VQ8 | Q95VQ8 franklini | 933 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 861 | 3.1 | 334 | 5 | Q95VQ9 | Q95VQ9 franklini | 934 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 862 | 3.1 | 334 | 5 | Q95VQ10 | Q95VQ10 franklini | 935 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 863 | 3.1 | 334 | 5 | Q95VQ11 | Q95VQ11 franklini | 936 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 864 | 3.1 | 334 | 5 | Q95VQ12 | Q95VQ12 franklini | 937 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 865 | 3.1 | 334 | 5 | Q95VQ13 | Q95VQ13 franklini | 938 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 866 | 3.1 | 334 | 5 | Q95VQ14 | Q95VQ14 franklini | 939 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 867 | 3.1 | 334 | 5 | Q95VQ15 | Q95VQ15 franklini | 940 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 868 | 3.1 | 334 | 5 | Q95VQ16 | Q95VQ16 franklini | 941 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 869 | 3.1 | 334 | 5 | Q95VQ17 | Q95VQ17 franklini | 942 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 870 | 3.1 | 334 | 5 | Q95VQ18 | Q95VQ18 franklini | 943 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 871 | 3.1 | 334 | 5 | Q95VQ19 | Q95VQ19 franklini | 944 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 872 | 3.1 | 334 | 5 | Q95VQ20 | Q95VQ20 franklini | 945 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 873 | 3.1 | 334 | 5 | Q95VQ21 | Q95VQ21 franklini | 946 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 874 | 3.1 | 334 | 5 | Q95VQ22 | Q95VQ22 franklini | 947 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 875 | 3.1 | 334 | 5 | Q95VQ23 | Q95VQ23 franklini | 948 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 876 | 3.1 | 334 | 5 | Q95VQ24 | Q95VQ24 franklini | 949 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 877 | 3.1 | 334 | 5 | Q95VQ25 | Q95VQ25 franklini | 950 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 878 | 3.1 | 334 | 5 | Q95VQ26 | Q95VQ26 franklini | 951 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 879 | 3.1 | 334 | 5 | Q95VQ27 | Q95VQ27 franklini | 952 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 880 | 3.1 | 334 | 5 | Q95VQ28 | Q95VQ28 franklini | 953 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 881 | 3.1 | 334 | 5 | Q95VQ29 | Q95VQ29 franklini | 954 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 882 | 3.1 | 334 | 5 | Q95VQ30 | Q95VQ30 franklini | 955 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 883 | 3.1 | 334 | 5 | Q95VQ31 | Q95VQ31 franklini | 956 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 884 | 3.1 | 334 | 5 | Q95VQ32 | Q95VQ32 franklini | 957 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 885 | 3.1 | 334 | 5 | Q95VQ33 | Q95VQ33 franklini | 958 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 886 | 3.1 | 334 | 5 | Q95VQ34 | Q95VQ34 franklini | 959 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 887 | 3.1 | 334 | 5 | Q95VQ35 | Q95VQ35 franklini | 960 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 888 | 3.1 | 334 | 5 | Q95VQ36 | Q95VQ36 franklini | 961 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 889 | 3.1 | 334 | 5 | Q95VQ37 | Q95VQ37 franklini | 962 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 890 | 3.1 | 334 | 5 | Q95VQ38 | Q95VQ38 franklini | 963 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 891 | 3.1 | 334 | 5 | Q95VQ39 | Q95VQ39 franklini | 964 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |
| 892 | 3.1 | 334 | 5 | Q95VQ40 | Q95VQ40 franklini | 965 | 6 | 3.1 | 16 | Q83QY7 | Q83QY7 shigella fl |

| | | |
|------|--------|-------------|
| 966 | Q8r770 | thermoanaer |
| 967 | Q8t2b8 | dictyosteli |
| 968 | Q8g94 | artirobacte |
| 969 | Q98443 | miscococcu |
| 970 | Q9nt1 | oryza sativ |
| 971 | Q7zv56 | brachydanio |
| 972 | Q813j7 | plasmodium |
| 973 | Q8mpn9 | euplotes ae |
| 974 | Q55938 | synecocyst |
| 975 | Q9ke08 | bacillus ha |
| 976 | Q9zax7 | streptomyc |
| 977 | Q824v1 | chlamydophi |
| 978 | Q84f7 | arabidopsis |
| 979 | Q7xst2 | oryza sativ |
| 980 | Q8en19 | oceanobacil |
| 981 | Q8z860 | salmonella |
| 982 | Q9zqa9 | arabidopsis |
| 983 | Q85154 | orientobilh |
| 984 | Q8zxp6 | pyrobaculum |
| 985 | Q7yld9 | oryza sativ |
| 986 | Q8mvd3 | caenorhabdi |
| 987 | Q25705 | plasmodium |
| 988 | Q25706 | plasmodium |
| 989 | Q9u6c4 | plasmodium |
| 990 | Q8y369 | raletonia s |
| 991 | Q93hf7 | streptomyc |
| 992 | Q7u9f6 | synecococc |
| 993 | Q8tt12 | methanosarc |
| 994 | Q26019 | plasmodium |
| 995 | Q8w0d1 | oryza sativ |
| 996 | Q9jt20 | neisseria m |
| 997 | Q8pgc3 | xanthomonas |
| 998 | Q83kv7 | shigella fl |
| 999 | Q82jx3 | streptomyc |
| 1000 | Q7v4u4 | prochloroco |

ALIGNMENTS

| | | | | |
|-----------------------|---|--------------------|---------------|-------------|
| RESULT 1 | Q8VC81 | PRELIMINARY; | PRT; | 195 AA. |
| ID | Q8VC81 | | | |
| AC | Q8VC81 | | | |
| DT | 01-MAR-2002 (TremBLrel. 20, Created) | | | |
| DT | 01-WAR-2002 (TremBLrel. 20, Last sequence update) | | | |
| DE | 01-OCT-2003 (TremBLrel. 25, Last annotation update) | | | |
| RIKEN | cdna 2010002E04 gene. | | | |
| GEN | 2010002E04RIK. | | | |
| Mus | musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Liver; | | | |
| RA | Strausberg R.; | | | |
| RL | Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; BC021592; AAH21592.1; - | | | |
| DR | MGD; MGI:1917086; 2010002E04RIK. | | | |
| DR | GO; GO:0005509; F:calcium ion binding; IEA. | | | |
| DR | GO; GO:0004623; F:phospholipase A2 activity; IEA. | | | |
| DR | GO; GO:0016042; P:lipid catabolism; IEA. | | | |
| DR | InterPro; IPR000886; ER_target_S. | | | |
| DR | InterPro; IPR001211; PhospholipaseA2. | | | |
| DR | PROSITE; PS00014; ER_TARGET; 1. | | | |
| SQ | SEQUENCE 195 AA; 21722 MW; 83A8E656ED08DA24 CRC64; | | | |
| Query Match | 19.6%; | Score 38; | DB 11; | Length 195; |
| Best Local Similarity | 100.0%; | Pred. No. 8.4e-32; | | |
| Matches | 38; | Conservative 0; | Mismatches 0; | Indels 0; |

| | | | |
|-----------------------|--|--------------------------------------|--------------|
| Db | 100 | SMDLGPAMTKCCNQLDVCYDTGANKYFCDAKFRWCL | 137 |
| RESULT 2 | | | |
| Q7ZTY1 | | | |
| ID | Q7ZTY1 | PRELIMINARY; | PRT; 180 AA. |
| AC | Q7ZTY1 | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Created) | | |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | |
| DE | Similar to phospholipase A2, group XIII. | | |
| OS | Brachydanio rerio (zebrafish) (Danio rerio). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; | | |
| OC | Cyprinidae; Danio. | | |
| OX | NCBI_TaxID=7955; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Body; | | |
| RA | MEDLINE=22388257; PubMed=12477932; | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | |
| RA | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | |
| RA | Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., | | |
| RA | Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., | | |
| RA | Jones S.J., Marra M.A.; | | |
| RT | "Generation and initial analysis of more than 15,000 full-length human | | |
| RT | and mouse cDNA sequences." | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Body; | | |
| RA | Strausberg R.; | | |
| RL | Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC052113; AAH52113.1; - | | |
| DR | GO; GO:0005509; F:calcium ion binding; IEA. | | |
| DR | GO; GO:0004623; F:phospholipase A2 activity; IEA. | | |
| DR | GO; GO:0016042; P:lipid catabolism; IEA. | | |
| DR | InterPro; IPR000886; ER_target_S. | | |
| DR | InterPro; IPR001211; PhospholipaseA2. | | |
| DR | PROSITE; PS00014; ER_TARGET; 1. | | |
| SQ | SEQUENCE 180 AA; 19975 MW; F44C2620B5690A601 CRC64; | | |
| Query Match | 6.7%; | Score 13; DB 13; Length 180; | |
| Best Local Similarity | 100.0%; | Pred. No. 2.8e-05; | |
| Matches | 13; Conservative 0; | Mismatches 0; Indels 0; Gaps 0; | |
| QY | 166 | NTWTLGCRPFNN | 178 |
| DB | 152 | NTWTLGCRPFNN | 164 |
| RESULT 3 | | | |
| Q8XGL7 | | | |
| ID | Q8XGL7 | PRELIMINARY; | PRT; 321 AA. |
| AC | Q8XGL7; | | |
| DT | 01-MAR-2002 (TrEMBLrel. 20, Created) | | |
| DT | 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | |
| DE | Putative lipoprotein transmembrane. | | |
| GN | RSP1355 OR RS04819 OR RSP1324 OR RS05678. | | |

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|----|-----|---------------|-----|
| QY | 166 | NTVWTLGCRPFMN | 178 |
|----|-----|---------------|-----|

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|----|-----|---------------|-----|
| Db | 152 | NTVWTLGCRPFMN | 164 |
|----|-----|---------------|-----|

RESULT 3

| | | | |
|--------|---|------|---------|
| Q8XGL7 | PRELIMINARY; | PRT; | 321 AA. |
| ID | Q8XGL7 | | |
| AC | Q8XGL7 | | |
| DT | 01-MAR-2002 (TremBLrel. 20, Created) | | |
| DT | 01-WAR-2002 (TremBLrel. 20, Last sequence update) | | |
| DE | 01-OCT-2003 (TremBLrel. 25, Last annotation update) | | |
| DE | Putative lipoprotein transmembrane. | | |
| GN | RSPI355 OR RS04819 OR RSPI324 OR RS05678. | | |

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DR  TIGRFAMs; TIGR00711; efflux_EmrB; 1.
DR  PROSITE; PS00850; MFS; 1.
DR  PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
DR  Transmembrane; Complete; Proteome.
SQ  SEQUENCE 484 AA; 48820 MW; 48820 MW; APCBF0EEB99CD415 CRC64;

Query Match      4.1%; Score 8; DB 16; Length 484;
Best Local Similarity 100.0%; Pred.No.13;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps

QY  13 SLGGGLAQ 20
DB  105 SLGGGLAQ 112
      |||||
      |||||

RESULT 5
Q9L004 PRELIMINARY; PRT; 489 AA.
ID  Q9L004
AC  Q9L004;
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  Putative transmembrane transport protein.
DE  SCO2309 OR SCC30.17C.
GN  Streptomyces coelicolor.
OS  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC  Streptomycineae; Streptomycetaceae; Streptomyces.
CC  NCBI_TaxID:1902;
[1]
EN  SEQUENCE FROM N.A.
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2);
RA  Seeger K.J., Harris D.;
RL  Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[2]
EN  SEQUENCE FROM N.A.
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2);
RA  Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL  Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[3]
EN  SEQUENCE FROM N.A.
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2);
RA  Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA  Knashi H., Hopwood D.A.;
RT  A set of ordered cosmids and a detailed genetic and physical map for
RT  the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL  Mol. Microbiol. 21:77-96 (1996).
[4]
EN  SEQUENCE FROM N.A.
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2) / M145;
RX  MEDLINE=21996410; PubMed=12000953;
RA  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA  Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA  Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA  Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA  Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA  Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA  Seeger K., Saunders R., Sharp S., Squares S., Taylor K.,
RA  Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA  Hopwood D.A.;
RT  "Complete genome sequence of the model actinomycete Streptomyces
RT  coelicolor A3(2).";
RL  Nature 417:141-147(2002).
DR  EMBL; AL939112; CAB88187.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0005215; F:transporter activity; IEA.
DR  GO; GO:0006810; P:transport; IEA.
DR  InterPro; IPR004638; Eflux_EmrB.
DR  InterPro; IPR007114; MFS.
DR  InterPro; IPR005828; Sub_transporter.
DR  Pfam; PF00083; sugar_tr; 1.
DR  TIGRFAMs; TIGR00711; efflux_EmrB; 1.
DR  PROSITE; PS00850; MFS; 1.

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Transmembrane; Complete proteome.
 SEQUENCE 489 AA; 49197 MW; C8013FC0B232E52F CRC64;
 Query Match 4.1%; Score 8; DB 16; Length 489;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 13 SGGGLAQ 20
 |||||
 107 SGGGLAQ 114
 RESULT 6
 Q7WL74 PRELIMINARY; PRT; 497 AA.
 ID Q7WL74
 AC Q7WL74;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative aldehyde dehydrogenase.
 GN BB1875.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 NCBI_TaxID=518;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=RB50 / ATCC BAA-588;
 RC MEDLINE=22827954; PubMed=12910271;
 RX Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";
 Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640442; CAE32372.1; --
 KW Complete proteome.
 SQ SEQUENCE 497 AA; 53676 MW; D2F05173AA568403 CRC64;
 Query Match 4.1%; Score 8; DB 16; Length 497;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 150 FVSKVEAC 157
 |||||
 318 FVSKVEAC 325
 RESULT 7
 Q7WT74 PRELIMINARY; PRT; 497 AA.
 ID Q7WT74
 AC Q7WT74;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative aldehyde dehydrogenase.
 GN BPP2426.
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 NCBI_TaxID=519;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=12822 / ATCC BAA-587;
 RC MEDLINE=22827954; PubMed=12910271;
 RX Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";
 Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640430; CAE37722.1; --
 KW Complete proteome.
 SQ SEQUENCE 497 AA; 53676 MW; D2F05173AA568403 CRC64;
 Query Match 4.1%; Score 8; DB 16; Length 497;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 150 FVSKVEAC 157
 |||||
 318 FVSKVEAC 325
 RESULT 8
 Q7WPF4 PRELIMINARY; PRT; 497 AA.
 ID Q7WPF4
 AC Q7WPF4;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative aldehyde dehydrogenase.
 GN BP2303.
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 NCBI_TaxID=520;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=Tobama I / ATCC BAA-589 / NCTC 13251;
 RC MEDLINE=22827954; PubMed=12910271;
 RX Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";
 Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640417; CAE42576.1; --
 KW Complete proteome.
 SQ SEQUENCE 497 AA; 53633 MW; E84BE6B75ED9B0EB CRC64;
 Query Match 4.1%; Score 8; DB 16; Length 497;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 150 FVSKVEAC 157
 |||||
 318 FVSKVEAC 325
 RESULT 9
 Q9C6J7 PRELIMINARY; PRT; 528 AA.
 ID Q9C6J7
 AC Q9C6J7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)

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DR GO: 0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro: IPR003959; AAA_Alipase_centri.
DR InterPro: IPR003960; AAA_sub.
DR InterPro: IPR000642; Peptidase_M41.
DR Pfam: PF00004; AAA; 1.
DR Pfam: PF01434; Peptidase_M41; 1.
DR PROSITE: PS00674; AAA; 1.
DR PROSITE: PS00674; AAA; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 603 AA; 67184 MW; A2DE7D2C930AAE23 CRC64;

Query Match 4.1%; Score 8; DB 16; Length 603;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AEEKEEL 194
DB 166 AEEKEEL 173

RESULT 11
QY815 PRELIMINARY; PRT; 637 AA.
AC QY815;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical C2H2 zinc finger protein.
GN SPBC1105.14.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-1.
RA McDougall R.C., Rajandream M.A., Barrell B.G., Ramsperger U.,
RA Bothe G., Fohl T;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096851; CAB50977.1; -.
DR PIR; T39291; T39291.
DR GenDB.SPombe; SPBC1105.14; -.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 637 AA; 69079 MW; C63CA05E448624AE CRC64;

Query Match 4.1%; Score 8; DB 3; Length 637;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 SDLKRSIG 149
DB 279 SDLKRSIG 286

RESULT 12
QY815 PRELIMINARY; PRT; 768 AA.
AC QY815;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN F8A12.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

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SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLINE=21016719; PubMed=1130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
Nature 408:816-820(2000).
EMBL; AC079284; AAG50939.1; -;
PIR; C96545; C96545.
HYPOTHETICAL PROTEIN.
SEQUENCE 768 AA; 88414 MW; F52E5065E2BA23AA CRC64;
Query Match 4.1%; Score 8; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
YF 7 FLVWLSSL 14
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Db 214 FLVWLSSL 221
RESULT 13
C Q80X16 PRELIMINARY; PRT; 5035 AA.
D Q80X16;
A 01-JUN-2003 (TrEMBLrel. 24, Created)
T 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E Ryanodine receptor.
N RYR1.
S Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
P SEQUENCE FROM N.A.
C STRAIN=BALB/cx3D-1F1;
A Kraev A., Kraev N., MacLennan D.H.;
T "Complete transcript sequence and strain-specific polymorphisms of the
T Ryrl gene of the house mouse";
T Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
R EMBL; AY268935; AAF29991.1; -;
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0005262; F:calcium channel activity; IEA.
R GO; GO:0005509; F:calcium ion binding; IEA.
R GO; GO:0004872; F:receptor activity; IEA.
R GO; GO:0006816; P:calcium ion transport; IEA.
R GO; GO:0006812; P:calcium ion transport; IEA.
R InterPro; IPR000699; Ca-rel_channel.
R InterPro; IPR01682; Ca/Na_pore.
R InterPro; IPR002048; EF-hand.
R InterPro; IPR005821; Ion_trans.
R InterPro; IPR003608; MIR.
R InterPro; IPR001215; Ryanodn_receptor.
R InterPro; IPR003032; RYR.
R InterPro; IPR003877; SPRY_receptor.
R Pfam; PF00520; ion_trans; 1.
R Pfam; PF02815; MIR; 3.

DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RYR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PRO0795; RYANODINER.
DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
KW Receptor.
SQ SEQUENCE 5035 AA; 565034 MW; D590990FA5846B76 CRC64;
Query Match 4.1%; Score 8; DB 11; Length 5035;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 AEEKEEL 194
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Db 1916 AEEKEEL 1923
RESULT 14
Q984N0 PRELIMINARY; PRT; 49 AA.
AC Q984N0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr7929.
GN MSR7929.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003013; BAB53599.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 49 AA; 5601 MW; 64D3E860FIADC82B CRC64;
Query Match 3.6%; Score 7; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 FLELLGG 59
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Db 26 FLELLGG 32
RESULT 15
Q8YMR5 PRELIMINARY; PRT; 63 AA.
AC Q8YMR5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Asl4865.
GN Asl4865.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RL Cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003597; BAB76564.1; --
 DR PIR; A12413; A12413.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 63 AA; 7615 NW; E86A0688CE22DE79 CRC64;

Query Match 3.6%; Score 7; DB 16; Length 63;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 YFLGLKV 97
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 Db 54 YFLGLKV 60

Search completed: May 17, 2004, 10:53:00
 Job time : 86 secs